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(21) International Application Number: PCT/US97/20313 (22) International Filing Date: 5 November 1997 (05.11.97) (30) Priority Data: 60/030,455 6 November 1996 (06.11.96) US (71) Applicant (for all designated States except US): WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Massachusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA). (74) Agents: GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		(81) Designated States: JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,
5 the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,
10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and
15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In
20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism
25 (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the

20 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

25 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

30 As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$ is the probability that two random individuals have the same polymorphic or allelic form at a given

- 5 polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote: $p(AA) = x^2$
 Homozygote: $p(BB) = y^2 = (1-x)^2$
 Single Heterozygote: $p(AB) = p(BA) = xy = x(1-x)$
 Both Heterozygotes: $p(AB+BA) = 2xy = 2x(1-x)$

- The probability of identity at one locus (i.e., the
 15 probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

- These calculations can be extended for any number of
 20 polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

- 25 $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

- The cumulative probability of identity (cum $p(ID)$) for each of multiple unlinked loci is determined by multiplying
 30 the probabilities provided by each locus.

$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ),

20 ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate
5 of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod
10 score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared.
15 Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

20 The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some
25 nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component)
30 except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,

5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

[illegible]

WI-9651b	105	A T ---			TCCTACATTCTATGGACAACCTCCATGCCCTTGGACATGCTGATCCCTCCTCCTCGGAATTCCTTCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCCTTCA/ATJGGGGCAGCTTGCAAGCCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCCCTCTG TCCTTAAACCTGTAAATGGTATATTAAATCCCTTGGTGTGTAATGTCCTC
WI-9651	139	T C ---			TCCTACATTCTATGGACAACCTCCATGCCCTTGGACATGCTGATCCCTCCTCCTCGGAATTCCTTCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCCTTCAAGGGGCGAGCTTGCAAGCCCTCCCTTTAGACACCT CT/CJACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCCCTCTGT CTTAAACCTGTAAATGGTATATTAAATCCCTTGGTGTGTAATGTCCTC
WI-7676b	309	A C ---			GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTCTCTTGGTGGCTGCTGGTGGAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139	C T ---			GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGCTGCTGGGACTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GC/CJGGCTCTCTTGGTGGCTGCTGGTGGAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGCAGTATAGGAGAGAGCAAGGATT
WI-10072	105	G A ---			CATTATCTTGCTCTGGGCTGTTCATTACCTTCTCCTCCTCCTCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGATTTTGAATATTTTGGTGA/JTGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAAGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T C ---			TTGGTGTGAACCTCAGAAATATAGGGAAAAAAGACAATTTGAA/T/A,CJGTACCCAGGAAACAAGAG CCCTGCACCTGACTCCAAAGGAGTTCTATTATCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCAICATCTGATCCAGGTAGTACTCACAAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACCTTATTGCAATT
WI-7041	174	C A ---			GTCTATTGCGAGGAGAAACGTCCCTTGCCACTCCCACTCTCATCAGGCCAAGTGGAGCTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAAGGGTCCCTCGGCTTTTATTT CAGGGCTTGCATGCGCTCTATTCCCTCTGCTCTC/CJCCACCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCATTTGTACAGTGTCTGTTCATGTAATAA
WI-7224	134	T C ---			ATAAACCCCTTGCTATGTATCACCCCAACTCACATTAATTATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCAGCTTATTTTGAAGAAAAATCCTAAACATCAAAATACCTTCATCCATAAAAAATGTACGATTJ /CJATTAATAAACAAATAACTTTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAAAATAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGATTGCTAG

WI-10826	132 A C ---	---	TCTATTTCACAGTAGCCCCATGAAGTAGGTAGGTATAACCCAGCCTCTATTTTAAATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAAGCAAAGACCTGCAIAC JCCCTGGCTTCCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGTGTGTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCCAC
TIGR- A004S25	145 G A ---	---	AGATCTGCCATTAGTATTTATTCCTTTGAAGATACTTTGGAGATTCATTTTCTTGAGTGGCAGTGCAT GCTCATTCAGTGAAAACCTTGTGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAAACCATCACCTGGTTTGCACTTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	AAACACACAGAATCATCAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAAATAGTAGGATAGTATTAATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACCTCTCCGTACTGTAATTTTCATTCTATGGAACCTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGTC TTTCAATAAAAAGAGTGACATGATTGAACATGTGTTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	TTCAATTCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTAATTCATTCAACAATTCGTCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCTTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	TTCAATTCCTTCCAAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTTGGGTGTGAGCGGATT AT[G/A]JCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTAATTCATTCAACAATTCGTCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATTCCTTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	TCAACACGCCTTTATTGCCACTTCTGGCTCCCTCTGTCGCCAGCAAGATTCCTACCTTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCCTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCTGCTTGTCTGGAGAGGGAGGGCCAGACAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACCTTCT[G/C]ACTGCAGAGTATAGGGACCAAGGTTCCAAACTTT
WI-9484	178 G A ---	---	TCAACACGCCTTTATTGCCACTTCTGGCTCCCTCTGTCGCCAGCAAGATTCCTACCTTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCCTTCTCCTCTGCACACTGCCAAGT TAAAGAAAACCTGCTTGTCTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACCTTCTGACTGCAGAGTATAGGGACCAAGGTTCCAACTTT

II-7330	207 C T ---			AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTTTTAAATGTGGCATATAGGTTT GTGACACAAGAAGTCATACCTTTGGTGGCTAAGTTTACTAAGGAAATAAATGAAAGATTAAAAAG TGAGAGTC/TTGAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTACAG
II-9443	211 G A ---			TTAAACAGTTCAGGTTGGTGAAGCAGAAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACCTT GCACAATTAATCCTCTTGGCATCATACAACTGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC/GA/CAGAGAGACCTTGGACTACAGATGACACCCACATGCCACTT
VI-7166	59 C T ---			TCCTCAAAAAGAGAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA/C/TTGGAT CATCAACAAGATTTCCCTTGTGCAAAATATTTGACTATTTCTGTATCTTTCACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAAACTTGTGTGTAACAATTTGTCGAAAGAGTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
VI-7259b	189 T C ---			GCTTCTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGGGGAGCAATTTTAGCC CCACCTGTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTCTCTCTGGCT GCGAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG/TT/CTGGGGGAGCAG AGCCAGCAGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGCTC
VI-7259	188 G T ---		C	GCTTCTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGGGGAGCAATTTTAGCC CCACCTGTCCCATCTGCCCCCTGCAACAGCTGCAGGCTGCTTCTCTCTGAGTCTCTCTGGCT GCGAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG/C/C/TTTGGGGGAGCA GAGCCAGCAGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGC
VI-7322	275 A G ---			GTACTTTAGGCCTGTGGAGGGTGGGCATTTAGTGTGACCTTGCACCAGGGTTTCTAACAGATGAC CCTGTGAATCATAAATTAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAATGCCTAAGCACTCAGGCCCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGGCCCTCTGGCTG
VI-7685	46 T C ---			TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTC/TT/CTTTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGTCTTGGAGCTGAGCCCTCTCACCTGTACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCCATGGCTTCTCTCCCTCTCCCTGCGGACTC CTGGTTGAGCTGTTGCCCTAGTCCCAACAGATGCTTTCTGTCTC
VI-563	87 G A ---			TGTGACCAATGTTATTTAGAGGGTTTAAACAATGGCCTGACTATCACCTGATGTGCGCCAGAAATTC CTGGGGAGGGCTCCCTT/GA/CCCTGATCATGTCTACCTAACTGCCTACTCTAACAAATACTACTCC TGTGGTATGGGATCCTAAGCCCAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCCAAATTTAAATCTCTTTGGATAACCCAGGGGCACAT

WI-931c	191	C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCCTTATCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATGTCCAAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[A/G]TCCCTCACCACACCTTCCAGTGCCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATGTCCAAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACGTGCTACTGTTGTATGGATTATAATTATGTCCAAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAATAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACCTACTTAG[A/G]CAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGACCTGTACTCTGTATACAAATAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCATTAAATAACGTTGCCCCCCC
WI-7719b	281	T C ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATCTAGCAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATTCTCCAGATGACCAGCAGTAGACAAATGGATCTAGCAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATATCTAACTGTGGCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTCTTCTTTTGTTA TGCCATTTGAGGGATTGATGTTCTTAAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAACACACTTTGT

NI-10673	94 C G ---	---	TCCCTTTATGCACCCAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGTGGCACTCATGGAGGGG[C/G]TCAGGTGGAACATATGCAGTGTCTCCGGCCACACA TCCTGCTGGGCCCCCTACCCTGCCCAATTCATCCTGCCAATAATCCTGCTTATTGTTTCATCCTG GAGAAATTGAAGGGAGGTCAAGTTGTTTGTCATGATTTGTCAGAGAACCT
NI-7842	57 T C ---	---	CACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGCTGAATCCCCTATCCCATTCTGTC/GTATGAG TCCCATTGGCTTGCAATTAGCATTCTGTCTCCCCCAAAAAGAAATGTGCTATGAAGCTTTCTTTCCCT ACACACTGTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGTAGTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAAATGATTACGCTCCCTTATA
NI-7721	145 A C ---	---	CTGCCATCACGCCCACTGGAGTCCACACTTGAATTTGGGAGCTACACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGCCACATCCCCACCCAGCTGTACCCAGCCGGGAGGTGCAGCCCTTCTCTCCC TGCTCTGC[A/C]TCTGACTCTCTTTGAGGTCCCTGTATGCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCTCTACTGGGGCTGGGGCTCTAGCCCCAA
NI-4767b	173 C A ---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCCCT CAGGTCTGGGTAATCCTAGATCTTCCCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATTCCTACTAAGA CTCCTCTAACCCAGAGATTTTAACT
NI-4767	50 A G ---	---	TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAAGATGCTCTTAGACTGA[A/G]ATTCTATAAAGAGTT CCTCAGGTCTGGGTAATCCTAGATCTTCCCTATATCCATTGAGTGTGATGGAGTTGGAGAGAGGGTATG TTCTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCCTACTAAGAC TCCTCTAACCCAGAGATTTTAACT
NI-7718f	222 C T ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGATG ACTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAT
NI-7718e	60 T C ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
NI-7718d	31 G A ---	---	ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT

II-7718c	91 C G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT
II-7718b	248 A G ---			ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATT[A/G]AT
II-7718a	42 A T ---	C		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGC[A/C],TGTACTCCCTACACTGATGC AAGGATTACAGAAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAAGAGGTGAAAATGAAGAAGGAAAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTA
II-7227d	99 G C ---			AGGGAATTGTGTTGCTCTGAGGAAGCCAGGCATCAATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGACCAATTCACTTTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCAATTGCTGCTTTCAACCAGCGACTAATG
VI-7227c	291 G A ---			AGGGAATTGTGTTGCTCTGAGGAAGCCAGGCATCAATTAAACAAGCCAGTAGGTCACTGGCTTC CGTGACCAATTCACTTTTCAGACAAG[C/G]TCTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCAATTGCTGCTTTCAACCAGCGACTAATG
VI-7227b	93 G T ---			AGGGAATTGTGTTGCTCTGAGGAAGCCAGGCATCAATTAAACAAGCCAGTAGGTCACTGGCTTC TTCCGTGGACCAATTCACTTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGACTGAGCTAAACA GTGTTATTATGGAAAGGAAATGGCAATTGCTGCTTTCAACCAGCGACTAATG
VI-7227a	24 A G ---			CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGTGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTATCCTTCATCGAACAAACTGATCGGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACCTGAGCCAAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCTGCCCATCCCA[A/C]ATGATCTTGAGATTTC

VI-7310a	64 T A ---	---	CCACAATGCCCTCTCCACGATGCAAGGACTCCTGTCTGTCTCTGGAGGTGGGAGACAAAGGAACCT/A CCGAAGAGGAGGAAAGCAAGCCGTACTGTCTATGTGTGATCCTTCATCGAACAACACTGATCGGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCCATCCCAATGATCTTGAGATTTC
VI-7878b	162 A G ---	---	CCAGCAACACCTACACCCCTTGTCACCTGCCCTGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGCCCTCCTGATAATCGCTCTGGGCATGATTGCAATGGAGGGCAATGCGTCC CTGAGGAGAAAATCTGGGAGGAGCTG[A/G]GTGTGATGAAGGTGATGTTGGAGGGAGCACAGTGT CTGTGGGGAGCCAGGAAGCTGCTACCCCAAGATTGGTGACGGAACCTA
VI-7878a	51 C G ---	---	CCAGCAACACCTACACCCCTTGTCACCTGCCCTGGACTCCTATGATGGCCTG[C/G]GTGTTGATAATAA TCAGATCATGCCCAAGACGGCCCTCCGATAATCGCTCTGGGCATGATTGCAATGGAGGGCAATGCG GTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGAGGGAGCACAGTG TCTGTGGGGAGCCAGGAAGCTGCTACCCCAAGATTGGTGACGGAACCTA
VI-7381c	213 C T ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTTCTTACC AGCCCTGCAAGTTTCTCATGGACGCTCGCGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAGATC AGATGTGGCCAAAGGAAGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAAGGCCCTC[C/T]GGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
VI-7381b	54 C G ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC[C/G]CTTTCTTTCT ACAGCCCTGCAAGTTTCTCATGGACGCTCGCGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAG ATCAGATGTGGCCAAAGGAAGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
VI-7381a	53 C G ---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCC[C/G]CTTTCTTTCT ACAGCCCTGCAAGTTTCTCATGGACGCTCGCGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAG ATCAGATGTGGCCAAAGGAAGAGCTCTGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
VI-1017b	93 G A ---	---	AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAA[G/A]GATGTAGATTGTACATTCAATCCTGAAACAACCTG CCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTTGTCCC
VI-1017a	92 G A ---	---	AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGAGCGAGGGAATTTGAACCTCTCTC AGGTACTGACTGTGGGACCAGACAA[G/A]GATGTAGATTGTACATTCAATCCTGAAACAACCTG CCAGGCAAGTCTTCTTCCCATTTTACAAATAAGGAGACAAAAATAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTTGTCCC

VI-1795b	130 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGCCTTTCAGAAAGAAAGT/C/C/C GTCACCATTTTCACCAAATTCGTAGTACAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
VI-1795a	47 T C ---	---	---	GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTT/C/C/TCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGCCTTTCAGAAAGAAAGT/C GTCTACCATTTTCACCAAATTCGTAGTACAATTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
VI-0616d	136 G A ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA C/G/ATAGCCCTCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
VI-0616c	136 G A ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA C/G/ATAGCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
VI-0616b	141 C T ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA CGTAGC/C/TCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
VI-0616a	116 G C ---	---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA CCACGTAGCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCCTGTTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
VI-1126c	52 G A ---	---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCAGT[G/A]TACTAATAAA AAACCCCTGTAAAGTCTGCTTGCAATTTCAAGATTCAATATATATATCCAGATTGTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTTCTCAAAAGGAATATGAAATT TGTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTTCTT
VI-1126b	230 T C ---	---	---	CTCTTATTTCTCTGGGCACCTGCTTTCTTTGGGGGCAAACTTCCAGTATCAGTATCAGTATATAAAAA CCCTGTAAAGTCTGCTTGCAATTTCAAGATTCAATATATATATATCCAGATTGTTTCCAGCAAGAAATT TTATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTTCTCAAAAGGAATATGAAATTGTT AAAATGCAATCCAGCTGTAACCTTTTTC/GGGACTTGCTTTTATTTCTT

VI-1126a	97 T C ---			CTCTTATTTCTGGGCACTGCTTTCTTTGGGGCAAACCTCCAGTATCACTGATACTAATAAAAA CCCTGTAAGTCTGCTTGCAATTTTCAAGAT[T/C]CAATATATATCCAGATTGTTTCCAGCAAAGAAA ATTTTATTTCTCAAGATATAAAAAATAAATATTTAAATTTTCAGTTTCTCAAAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTTCTT
VI-1183c	124 C T ---			TAGTGCTAAATTTTGGAAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTTGCCCTTGTCACCTAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
VI-1183b	192 T C ---			TAGTGCTAAATTTTGGAAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTTGCCCTTGTCACCTAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATTTAAATTTGGT ATGTGGTCTAGAGTTAGTAATGGAA
VI-1183a	118 C T ---			TAGTGCTAAATTTTGGAAAAAGTTTGCTGATTTTTAAAAATCTTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTTGC[C/T]CTTGTCACCTAACAA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTCTAGAGTTAGTAATGGAA
VI-10770b	174 G A ---			GCTTGGTTGCTTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTTCTGCCTGGCCCTTTTGATTTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCCCTATCTGAGCGCTCTTCCCTTGACTTTCTCCTG TTCACCAACCTTCTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGCTCCCTTTCCC
VI-10770a	49 G T ---			GCTTGGTTGCTTTAGTCTTATTGCTCAGTCTTGAGTTCTCCCTTTCT[G/T]CCTGGCCCTTTTGATTT TCACCCATACCTCTATGCCCTGCTCAGACCATTTCCCTATCTGAGCGCTCTTCCCTTGACTTTCTC CTGTTCAACCAACCTTCTTTTATTCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTCTGTGCTCCCTTTCCC
NI-9667b	82 C T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTTGATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCCAGCAGGCTTAGAACCTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCAATCT
NI-9667a	68 G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCCCTGCTCATGACACTTTTCAATCTCTGCCCTTGATCATG G/C]TTATCACTGGACACAGCCACCTCCCCAGCAGGCTTAGAACCTCCATGAGTAAGGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCAATCT

VI-0400d	189	A G ---			ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTAATTTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTG[A/G]TGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
VI-10400c	166	A C ---			ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTAATTTT TCITTCCTTACCTTTACTCTCCCAACCA[A/C]AAATAACGTAAGTACCTATGTGCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
VI-10400b	165	A G ---			ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAATTGCATTTTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTAATTTT TCITTCCTTACCTTTACTCTCCCAACCA[A/G]AAATAACGTAAGTACCTATGTGCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
VI-10400a	46	T C ---			ACATTTTATTAGCAACAAATCAGCAAAATAATAATAGAAAGTAAT[TC]TGCAATTTTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAAGCAGCTTACTAACACAATATTTTATTCTA ATTTTCTTTCCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTGCATGCCATGT AGTTTTTGGTTCAATTTACTTGCAAAATTATTCAAAGGCGTTAATGCATTATG
VI-10809b	78	C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCA[C/T]TAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
VI-10809a	33	C T ---			AAAGGGCTACAACTAAGGCCAAAAACCATGAAT[TC]TGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCACTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
VI-7038c	266	T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTGTAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAAGACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATTGAT CATTTTATAIGAAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
VI-7038b	140	A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATAGTGTAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTGAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCCTGCATTTATGGTGTAGTTCTG

I-7038a	31	G A ---	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATAGTCTGGGCTGCTCTCCCTCCAGGAATGCTGGCCCCCAGCCCTGGCCA GACAAAGAGACTGTCAGGAAGGTCGGAGTCTGTAACACAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAITATGGTGTAGTCTGA
I-3429b	64	G T ---	---	---	ATACGCTTCTGTCTGCCACAGTGAACACAGACCCAGGTGCCAGGGTCCGGCTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTGCATGTGTCCATCGGTGACTCAGACACAGAGTTTCCAACCTCATGTGA CAAAATACAGATTCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
I-3429a	62	C T ---	---	---	ATACGCTTCTGTCTGCCACAGTGAACACAGACCCAGGTGCCAGGGTCCGGCTCCACACA[C/T]AG CCCTCAGCCCCCTCAGCTTGCATGTGTCCATCGGTGACTCAGACACAGAGTTTCCAACCTCATGTGA CAAAATACAGATTCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
I-6786c	151	G A ---	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTGAGCCCCATTCT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTTC TTTTGGCAGGGGACACTCCTTCTGGTGCTCTATTGCTCAGTTTCATCATT
I-6786b	111	A T ---	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATTAAGAAAGTGAGTGACGGTGA CCTGTAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTTC TTTTGGCAGGGGACACTCCTTCTGGTGCTCTATTGCTCAGTTTCATCATT
I-6786a	106	A T ---	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAJA/TJGGATAAAGAGTGAGTGACGGTGA CCTGTAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAAATGCCACATTTC TTTTGGCAGGGGACACTCCTTCTGGTGCTCTATTGCTCAGTTTCATCATT
I-6711b	226	G T ---	---	---	GGCTATTGTAAATGCTTGGTTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCCTCTGAAT TTCATATACCTCCATTATTAATTCATACATCATTGCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTGGTGCCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
I-6711a	36	T C ---	---	---	GGCTATTGTAAATGCTTGGTTATTGACTCCAAA[T/C]TGAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAAACCTTCAGTTCCAATCCTCT GAATTCATATACCTCCATTATTAATTCATACATCATTGCAGAGAAAAGACACGGTGCCAACTG GGTTGGTGGTGCTGCACACCCACAGTGGCAACTAAGTGAATCTCTAAA

I- J613b	172 A C ---		ATTGTATGCCAAAATCATAATACCCCTGCAATCTAGAAACATACAGTGTAAATTTTGAGCCATA TGGTGAAAAATTTAGAAAGTATTATTCTCTATATGTATATACTACGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTG/C/GCCCTAGGAGGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
I- J613a	44 G A ---		ATTGTATGCCAAAATCATAATACCCCTGCATCTAGAAACATACA/G/ATGTAAATAGAAATTTGAGCC ATATGGTGAAAAATTTAGAAAGTATTATTCTCTATATGTATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
I-7587c	133 A T ---		GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA/A/ TGGAAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
I-7587b	81 G A ---		GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCTTCTG/G/ATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
I-7587a	28 C T ---		GCTCTAGTGGGAAACCTCAGGTAGCTCCCGAAGATCTGTGCTTTCCAAACAAGTGACTACCCCTTGA AGCACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAAATATCCCAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
I- J681b	103 T A ---		ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAAAC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC/T/AJAAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAAGGAGGTGACGCTCTGTTAAAG
I- J681a	41 A T ---		ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAACTTAATTCG TAGTTTATGATTTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAAGGAGGTGACGCTCTGTTAAAG
I-7222c	126 G T ---		GCCTCTCCTCAACTGTCTGGACCCAAAGGTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG/G/TAATAA AGGAGGGGGAATCCCTTGAACAAGAAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAGACTCGAATTCATTTT

lI-7222b	255	G A ---	---	GCCTCTCCTCAACTGTCTCTGGACCCCAAGGCTAGGAAAGGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGATGGGGAATAAAGG AGGGGGAATTCCTTTGAACAAGAAGAACTGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGGTTGTATTTCAAAGACTCGAAATTCATTTCTCA
VI-7222a	126	G T ---	---	GCCTCTCCTCAACTGTCTCTGGACCCCAAGGCTAGGAAAGGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGATGGG[G/T]AATAA AGAGGGGGAATTCCTTTGAACAAGAAGAACTGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTTGTATTTCAAAGACTCGAAATTCATTTT
VI-8054d	41	C A ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCCTTTC[A/T]ATCTCTCTCCAGTTCAAAATG CTTGCACTCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCGGGAAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCT TCCTGTCAACGCGCTTCCCTGGCGGTACAGAGATCCTTGCCCTT
VI-8054c	237	G T ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCCTTTCATCTCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCCTTAGCACAA TCTTCTTTGTAGTTTAGCCCTTTTCGGGAAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCTCC TGTCATAACGCGCTTCCCTGGCGGTACAGA[G/T]AATCCTTGCCCTT
VI-8054b	148	T C ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCCTTTCATCTCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCCTTAGCACAA TCTTCTTTGTAGT[C/T]TAGCCCTTTTCGGGAAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCT TCCTGTCAACGCGCTTCCCTGGCGGTACAGAGATCCTTGCCCTT
VI-8054a	131	C G ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCCTTTCATCTCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATTCCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCCTTAG[C/G]A CAATCTCTTTGTAGTTTAGCCCTTTTCGGGAAAATCGGCTTAGTTGCCCCACCATAGCCACTCTGCT TCCTGTCAACGCGCTTCCCTGGCGGTACAGAGATCCTTGCCCTT
VI-8054b	152	G T ---	---	TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAAACACGACGATAGTTAAACGCTGCTGTAAGTTTAT ACGGTGTGCGAGGCAACA[G/T]GGAGAGGTACGGGAATAGTTCTACTTCCCTGTTTTTATTCTTG TTTAGACACAGGCTGCTGTGTG
VI-8054a	102	C T ---	---	TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGCTGCTGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCCCTGTTTTTATTCTTG TTTAGACACAGGCTGCTGTGTG

I-9826b	127	G A ---	---	---	AATTTATATGTGAAGGGTTAGCAAACATAGGCCACAGGCCCAATCTAGCCATGCCTATTTTTGTG TGCCTGATGGCTGTTGGTGTTTGACGCGAGTTGAGCCATTGTGACAGAGGCTGTTATG/AGCCTT CAAAGCCAAAAAATAATTTACTCTCTGCGCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAA GGCAGAGAGATCAGAAGTGTGAA
I-9826	125	A T ---	---	---	AATTTATATGTGAAGGGTTAGCAAACATAGGCCACAGGCCCAATCTAGCCATGCCTATTTTTGTG TGCCTGATGGCTGTTGGTGTTTGACGCGAGTTGAGCCATTGTGACAGAGGCTGTTATJTGCCCTTC AAAGCCAAAAAATAATTTACTCTCTGCGCTTGACGGGAAAGTTTGCTGATTCTAGATATTTAAAG GCAGAGAGATCAGAAGTGTGAA
I-15986	60	T G GTGGTTTTT	TTGTTTGTGT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTTTTJ/GJTTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
I-8655	29	A G AG	AACTGCAAAAT AGGAAACCAG	CCACCTGGGGC TCCC	TTCAAGTAACTGCAAAATAGGAAACCAGAG/AGJGGGAGCCCCCAGGTGGGACAAATCATGGCTACCC TCCCCAACAGAACAGGGGGAGGAGGTGGCCCTACACCCTTTAT
I-8170b	259	G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTTAAGTACTCTACCAAGATGCTGTGGTAAGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
I-8170a	204	T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTTAAGTACTCTACCAAGATGCTGTGGTAAGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA A/T/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
I-8172	136	C G GACA	CCTTTATTA ATTGTTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGATCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCTTTATTAATAATTGTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTCTTACCCGTTTACA
I-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTTGTTGAAAT CAACCTGC	AGCAGGGTTGAAATTGATCCCTTATTTACATGAAATAAAAAAATTTCTGTTCG/G/AGCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTCGTTTCTGATGCAGGACAAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
I-14149	83	CT ---	---	---	GCCTTATTTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCAAGCATGGGATTTTGCCCGAAAT ATTAGCGTTAAAGGAG/C/TJGAGTTGAGTCAAAACACGGG
I-8712	44	G A G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG/G/AGATGGTCAGGCTTCCTG TTCCCTAACAGCAGAGCCCCAGCAACCTAGAAAGCCCTCACCTAGCCTCTTAAT

NI-8827	22	C T	TOOCTGGGAG ACTATGG	GCATTAGGAT TTTAGTGTTCA C	GGTGCCCTGGGAGACTATGG[C/T]AGTGAACACTAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACITTCITTAGTTCCTTCTTATCCACCCAGTCTTCT
NI-8833	51	A T	TCTTCATGCC ATTCTCTG	CCTCACACATT ATAGGGCA	CTCGGGCTCTTAAAGCTCTCTGTAGACTGTCTCTTCCATGCCATTCTCTG[A/T]TGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACGCTTGTGCATAAAAGGTCAGCTATGT
NI-8377	63	A G	---	---	ATTTTATGCCATGTTGGTAAAGTTCAITTTTTCAGTACATGGGTACACCCAGGCCCTTTCCCA[G/T] TATATCCAGGTATGCTACAAGTCTTTTAACTTATCAGAAGTTATTTACTGTTTCTTAGAGAG GCTACCAGGCTAAATTCACCTAGTTGGTTGTCTAATGTCTCATTTTATCCTGAAGCTCGTG
NI-8850	21	A G	GGGACTTAAC CTTTGGCT	CAACAGCCA GGCAGG	GAGGACTTAACCTTTGGCTT[A/G]CCTGCCTGGCTGTTGGCTCTGCGCTTGCTGTTTTGGTTCTT TCTCTTCTACTGGTCTTTCTTTGTCTTTGCCAGCCACCTATGCTGCTGT
NI-8853	79	C T	OCGGGCATTG AGGATA	AGTCTTCTGA GCCTTCCAT	ACTTTCTTGAGCTGAGCAACCTCATCTATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CAITGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTTCATTCTCAA
NI-8865b	52	A G	---	---	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTGTGTCGAACA[A/G]ACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAAA
NI-8865a	42	T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T/C]GGTCGAACAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAAA
NI-8895	32	A C	---	---	GTGCCACAAACCTGGACACCAACCAACAGAAT[A/C]TCCCGTCTTTGAAATTTCCATTAAAGACA CAATGGGGTAATTATACAGGGATGCTCCAATCGCTCTTTC
NI-8456	93	G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAATATAATAAAGTCTTTTCC AAGGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTGCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCACACGGCAGACCACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCGTCTCAGTCAACCCAC
NI-8496b	157	A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGAAA ATTTCATATCTCAAGTAAGTACTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGAC
NI-8496	41	G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAATGGTAATGTTGTATCAGTGCATATTCTATGG AAAATTCATATCTCAAGTAAGTACTAGCCTAGAAATCAGAGACAGCAGTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATAGTATATAGAAATAATACGAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGAC
NI-14153	28	A G	GTGAGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCTCTGCGCTTGTCAACCCACATCCACAGAGCA GCCCTAGTGCAGGTGCAGCAGTGCACCCACAGGGAACAGGACCCCAIGCTGC

352a	69	T C G	AGCACAGCAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTTCCAGAAAGGAGAGAGAGTCACTACATAAGCACAGCACATAGTGGAA AGTTC/GCTAAGTGTCTACGAGAGGTGAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTTGCA CACTTA
-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCCCTGA GCAC	TTAGCCCATGCTGTGTCATTTGCCATCACCTGTGAAACCTATGAAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGTC/GTGTCTCAGCGCGGGCTGGACATCCATGTTGGGAAGAGTTGCGCGGGT GATTCGATGCGTATAT
-11385	75	T C G T T T T	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTGGCCTGATGGTGACACAGAGACTTTTCATATTCCTGTTTTTAAAAAGTC TCTTCAGTC/JAGGAAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGATAAGAAATCAGC
-11388	88	C A A G T T C	TGTTTGAATTT ACACGTAACT	TGCCCTGTATC CAAGTTAAAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTTAAAGAATGAATGTTTTG AAATTACACGTAACTAAGTTC[C/A]TATAAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
-11392	55	T G A T A A A T A C	GGTTATGTGTT CTTGAACITTTA	GTACATTCACG TGTTTTGTAAA	TTCTATCATTCCTAAATGGGCAGGTTATGTGTTCTTGAACITTTAATAATACTC/GCTTTTTTACA AAACACGTGAATGTACTTTCTTGTCAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
-11396	52	A T T	TTTTGTTTTG AAATGGTGTTT	AGCTTATTTTC ATATTACCCCA	AAAGAAATAAGATGGCAATTTGTTTCAGTTAAATTTTGTGTTTGAATGGTGTGTTTATGATGGGTGAATA TGAAATAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTGATTTTGAACCGTTGTCAT
-11441	100	C A C A G C	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTGAGTCTTCCCCAACTAAACCGTGAGTCCAGTATGTCTGGCAGCAGTCTGTCTGTTCTTGGTG TATTTCCCATTAAGTGAATCCCAACCAACAGC[C/A]CAATAAGGCCCTGGCACAAAGTAAGTCTCTCC ATTTTGTAGAAATGAAT
-11466	26	C T T T T A T T T T G C A	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTTATTTTGCAGTC/JCTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTTCTATTATCTATTTATCTCTCAGACATACATTT CATGTATCCTG
-11364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTTTTTTAGTAGAAGC[A/G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAAAATGTCA
-11276	41	A G A G C A G A C	GGCAGCCAGG AGCAGAC	TGTACTGAGGA GOOGTG	AGGCAACACTGCTTTATTAGCGCGGCGCAGCCAGGAGAGAC[A/G]CACCGGCTCCTCAGTACACATT CCCCACCCCTGCTGCTGGTGTCTCCCACTCAGGGCTGGGCATGGAGGGGCGAGCTAGGCTCTGGAA
-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCAAT[A/G]GGAACAACATATGCAAACTAGCATCATTTGCTCTAGA
-186b	88	A G ---	---	---	AATGGTCTGTTTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAGACACATACGGTACAAAAATTACA GGTGGTTAGTTCATTACATG[A/G]TACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

36a	52	C T A	GGTCATTTGAT GGAAAGACAC	AACTAAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
2234	66	A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTTGGCTATAGGTCAGTGTCTAAACCTTGAGCTTGCAAGAGAACACTTGTGGGGCTT[A/ G]TTCAAACATGGACTGATAGGTCACCCCCAGATTTCTAACTGGGTAGGCTGGGGTG
2345	37	C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGCGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATCTCT TTCTGACCAGCTGGGCTTGGCACCTTTGTGAGATTTGCAAAA
13416	71	C A AAA	AAATTTTGG AAGTTTTTCAG	AGTGTATTATAG TTCAATGAATA ATTTCAA	GAAAAAGGCTGTAATTTTATTTTCAAATTTTGGAAAGTTTTTTCAGAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTTATTCATTGAACATAAACACTTAGCAGAGGAAAGGACTTTTGTAT
2310	46	G A AAAAGC	TTATTTCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGGTCT AAA	TTTGAAAAGATGCTGAATTTTATTTCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGGACCCCAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAATTTTACAAATATCCAGAAAGGCAATTTTCTTAAGCAG T
2086	72	C T TTGGATT	CCGGGAAAAAC TTGGATT	GGAGTCTCGG GTCTTGG	GAACCGAGCTTTATTGGAGCAAGAGAGTGTGGACACTGTTTACAACAAAACGTTTCCGGGAAAAACTTG GATTT[C/T]CCAAGACCCGAAAGACTCTCCTCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
1549	102	T G TTTTATG	GCATAAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCCC	ATGCTTTCACAGGTGTATTTTGTAAAGAGTTTGTCTATCTAAATTTTCATATTTATTTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG[T/G]GGGATTTGTACAGACTTTCCCTC
1585	79	T C AAACAAAA	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTC	TTAGAAGGAAAGAAATAAAACACGGTAATGGGAAATCAGTTTCAGAGGTAGGAAGGAGCTGGGTT TGCAAAAACAAAA[T/C]GGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAGAGCAGGGGTAGAGT TT
1604	68	G C ---	---	---	TTAGTTGGTTTCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACAGCATTTT G/CJAGAACTAGGGACTTTTCCATGAAATAAATAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
4c	108	C A ---	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAA[C/A]ATATTAAAGTATTCGTCAGCTAC GGACTTCGT
4a	60	A G CAGCTGCTTG	CCAGAAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATAATTAAGTATTCGTCAGCTAC GGACTTCGT
3b	83	T C ---	---	---	TTGATTTTACTAAGGCTTCCACTGGAAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAA[T/C]TACTTAAATAAGAAATTAGCCATACCACATTGTTCATTGCTAC AAGAACAAATTGGCAATGA

326a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGTCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTAAATAAAATTACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTGCTAC AAGAACAATGGCAATGA
11627	23	T C A T T G T C T C	CCTTCCCTCC CATCTCAAG	CATTTGCAACC CATCTCAAG	ACCCCTTCCCTCCATTGTCTCT[Q/C]CTTGAGATGGGTGCAAAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATAGTATGCTTTTGTCTGGCTTACTTCCATTGCGATGTCAAGTCCATCCATG
11636	61	A G T C C T	GGACTTAAAA AGATCTGCTTA T C C T	AGAAACTTGGT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAAGGTGGACTTAAAGAAATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCCTTTTGGTA
11537	119	C G T	ATTGCTCATCT TACTCTGACCA T	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAAATAATTTACAG TATACAATATTAGAGAATAATTATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATCTT TTTGCTGGGTCCAGGACC
11654	37	G C C T G	GCCAAAAGAC TATTCAGCAA C T G	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTACAGCAACTG[C/G]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTCAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGT
11656	28	G A A A	ATTGATTTTAG AAGGAACTGC A A	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAAGTCAA[G/A]CTTTACTTGAGGACAAAAGCCTTGCCCTGCAGTTGTTT AAATGTCTGAAACAATCAGATTCCAGCCTGGAT
11680	55	T C	---	---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCTTTT[C/T]TGCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
11696	47	T C A G G G A C A G	TTATCACAGC C A G G G A C A G	GGCATTAGAGA AGCCAACTT	GTCCAAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG[C/J]AAGGTTGGCTTCTCTA ATGCCACCATCTTGTTTTCAGAACTTTCCACTTCCGCT
11702	69	C T C A G C A G	GAATAATACT GAAATAACCA C A G C A G	AGAACAACCTT AAGCAAAATTAT ACTGAAA	TTACATGTGGTCAATGTGACATACTTTCAATAATTAATAAATCGAATAACTGAAATAACCAACAG AG[C/T]TTTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTGTCTGCAGA
11706	60	C T T C T C T C T	TGGCTGGAATT T C T C T C T	ATCACCAAAG AACAAATTCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTCTTGTGACAATTTATTTGC[C/T]GGCTG GAATTTGTCTTTGGTGATTGTCCCTTGTCTGT
11709	105	T A T T C A G T T T G C	AGAAGCTTGC T T C A G T T T G C	TCATTTCTCT AATTTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGAGTGTCTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAANA
11710	103	C A C A G T C T C A	GCACCTAGCCT C A G T C T C A	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCAAGCTTTCCAGCAACAACAGCCAGCCCACTCTAGACACGCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCAC[C/A]CTCCTCCCTCCCTCCACACACTCCTTC

'15b	123 C T	AGGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTCTTAGCCAC AGGATGGGACTGGGAAGA
715a	49 A C AAA	GCACACAATG TAAACAGAC AAA	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAAA[AC]TGCATTACAACCTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTACAGCCAC AGGATGGGACTGGGAAGA
-11727	43 G C TCAACA	AACAATCCTT AAAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTTATACCTAACAAATCCTTAAACAACTATCAACA[G/C]CTGCAACACAAAACACAGGC AAATGAAAAACAGATGCCCGAGACAGCACCCACACATGGCACACAC
-11728	16 C G ---	ATCTGTGGTTT TCGCTG	---	TTTTATTATCAAACT[C/G]CAATTCCATTTACAAAATGTAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTTCTTATCTCTTCCACCTTACACTTCTCTCCCTACAACCCGGGTTCCAAA
-11758	61 A G TCGCTG	GCCTCACAAA GTATTTCTAA	TGATTGGCCCT GTGGTCTA	TTTTCCCTCTTTTATTAAAGTCCGCTATACTAACTAGAGGAGAAATCTGTGTTTTTGGCTG[A/G]TAG ACCACAGGGCCCAATCACACAGCTTCTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
-11295	37 A G AATATA	GTATTTCTAA T	TCTGTGAACCTC T	CCGGCCTCACAAAAGTATTTCTAAATATAATTTGCT[A/G]TAGAGTTACAGATGAGCACTTTTCA CAITAGGIGATATGCAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
-11773	93 T C ---	GGCTCAGAGA GCAAGGGAA	---	AGCATGATATTTCTGCCTGGAGTTTCTGTGAGCTCAGCAAAACAGCAGAGTCAGAGATTAAAGAATT ATTTATGGCTCTCTTTTCTCCCT[C/G]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
-11282	42 C G GCAAGGGAA	GGCTCAGAGA GCAAGGGAA	AAAACCTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTATTTAATGGGCTCAGAGAGCAAGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTTGCGCGCAGAGACCCCTCTCCACCTTTTTCATGCTGTGTACACACACACTGTCCCAAGCCTC AGA
-11790	28 A G AAACCTCTG	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAACCTCTGT[A/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTTACAATGGGCAAAATCATCTAACACAAAGC
-11879	61 C A AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAGCTTACAACCATCTTTTCACTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTTCTTTTATAAAGTGAAGGTTCAACTATCCAGACAGTCCCATCTA
469b	91 C T AAGTTTAAA	GTITTTAATGT GGTATTAGAA AAGTTTAAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCATTTCTCCCTTTTATAGTTTTTAAATGTGTTATTAGAAAAAGTTTAAATTTACAT ATGTGGCTTATATTCTATTCTA[C/T]TTGACAGCACAGTTCTTCAAAGTTTGTATAGACAATCTGA AAATGGGTTCTGAACT
-11906	52 A G ATCTGAA	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAATCTGAAT[A/G]TGAGGGAACCTG CAGAAATTAACCTTCAGTCTAATCTCAGAAATGCCAGAGTAAGATGAACCCCTTTACAG

VI-11909	78	A	G	TTTGTTGGG TGGTCAAG	CTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTCTAAATGGCTATTTGTGTG GGTGGTCAAG[A/G]CTATTGAGAAAATCTCAGAGGAGGACAAATGATAGTGCACTGCAGCCAGCTCG GACTGGCTTGCAGAGTC
VI-11806	60	T	G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
VI-11946	31	C	A	---	---	CCCTAGTGAATACAACCTTTTGCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACCTCTCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGAGGGAA
NI-11965	65	T	G	TGAAGATCAG ATCTCTGGTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTTCTTGCTTGAAGATCAGATCTCTGGTTATTAA[T/ G]ATCAACATTACCACAGCTGAAGGAAATTAACCTGAACCT
NI-11027	90	T	A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTGAAACTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAT[A/A]AATAAAATCTGTAAACACATTTCTCATTTCTCTTACGA ATACTTCTTTTGATATTGCAAAATTTCTATGGCATAACAGAGGCACCTCTCAATGCCCCG
NI-11049	95	C	T	---	---	TTCTGCTGAAGATCACAAAACAAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTTGTACCTTT GTGTTTATTTCTGTTTCAACTAAGG[A/C]TAGACTTCAGAAGGCATAGCTTCCCCTTGTAACGTTTTT AAACATCTTTTTCAATTTGTAGGAAGGAACATTTCAAAAGCCCCA
NI-15488	69	C	T	AAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAAAACATGGTAGGGAAAAGTTCTCACTCTGCACATATAAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAAATTTTAAACAAATTG
NI-13654	49	A	G	AACAGTTAAT GAAACACATC CGT	GGCTGTGAAA TGATGTGAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACCTTTTCCCCATTTTACAGACAAAACCCAGT
NI-11070b	135	C	T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGAAAAGGAGCTAGGACAAATTTCTTGCTT TCAAGTAAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C[C/T]GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
NI-11070a	110	G	T	CAGAAAATCA GCCAGCTATCT	TTGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATAATGAAAAGGAGCTAGGACAAATTTCTTGCTT TCAAGTAAAATTTGTGACTGAGCAGAAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAACAGAAGGGAA
NI-12020	121	T	C	---	---	AATCTTTTATATTTCCAGCTGTTGAGACAGTATTTTGAGGGCTGATTTACCTCTAGCGCGGAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTTGTTCTCCTC

WI-11076b	142	G A ---	---		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCATGGCTTATCTTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA	TCCTGCTCTGG GTATGTGAC		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCATGGCTTATCTTTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCAT[G/C]GTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	GGTTATTCAAA AATTAGTATGG GACA		ACCTTTAAAGTTTCTCCACCTACTCCCGCAGAAAAGGCATATTCAA[T/C]GTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-14267	28	T C ---	---		AATTATTGCTGAAATTAGGAAGGAGCAT[G/C]TGAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAGTATAAACTCGTA
WI-13892	50	G A TAGAAC	CTTTTCATTTT TGCTTTTAAA ATCAAG		GATTTGTTTATTTCATTTCTCGCTTTTCAATTTTGCTTTTAAATAGAAC[G/A]CTTTGATTTTAGTA TATGACATCATCATGAAATTTTCTCTTACTTTGATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-15288	108	C G TCCCTCTCTC	CATGAGAGGA AAAAGCTTCTT TCCCTTGGA		ACCTCTTTCTGATGACACTGTACCTGTAGGGGTCTAGAGAGAAAGAGTAGTAGACTCCTACTTTGC TACAAATTCAGGATGCAGGCGATGAGAGGATCCCTCTCTC[G/C]GTCCAAAGGAAAGAGCTTTTGGC
WI-3951b	88	G C ---	---		AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAATAATTTACTGAACACTTGCTATGTGCTG G
VI-3951a	39	C T CAAAA	TTCCTCTGATC TGGGGTCT		AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAATAATTTACTGAACACTTGCTATGTGCTG G
II-13264	25	G A TTGCCCAT	GGAGGGAGAG ACGGAATA		GAGACCAAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCTCCCTCCTGACTGACCCAGTGTCTT ACAATGAACATCCCTCAGCCCCCATGGCATGGTGCATCCCTCTCTTTGGATCTGTGAATATAACCA ACTGTCTTGTCATGGC
II-13960	39	A C TGATAGA	CATGAAAGGA CAAAATTTGCAT C		TTATTGTCTATTAGCAAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAACTTGTTCACTGTCTTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
I-15843	62	C T CAG	CTCTGGCTCAG ACTTGCTCT		AACTCTTATTGTTTAGCTAGCCCCAGTGACTTTATGCACTCTTATAACCAAGAGCCTTCAG[C/T]AG AGCAAGCTGAGCCAGAGGTTTATCACACTTTGTCCCTCAGGGTCCACCAGGAACCCAGGCTTGGCT

VI-13983	52 G A	TCTCTCCACT CCITTAACCT	CAATACTCTCT TAGCCCAGTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACTGACTGACTTAACAGAAATTAGAACATCCAGGCACTCACTGAGA
VI-13850	51 A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGAAATAAATAAGATGGACTTCGAGGTGTAAAGATTACACTTCA
VI-15295	27 G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCTCTTTGCCAACTATTTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCGAAATATGAGTGAGACTCA
VI-14284	55 C T ---	---	---	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCCTTTAGTGCAAAACA[C/T]TATGCCAT GCGGAAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCAATTGA
VI-14288	85 G C	CCGCTGCTATT CCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAGCCCTGTTCTATATGAAGACAACAGGTGGCCATACITGGGTGGAGGGATA CCGCTGCTATTCAGAT[G/C]AAGATTTGGTGGAGGAGACCATGACAGATGACAAACGG
VI-13522	33 C T A C A A C	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTTG AAGTCAGTGGT TCTC	TTTATTTGTAGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACTGACTTCAATATTATGAGAG AAAAATTACTCCAGGGAATTTTTCAGAGAAGATAATA
VI-13529	42 T C T T A C C A	CACAAACATT TATTGAACAG TTACCA	TCTATACACTT CTCACTCTCTT GCTT	AAATATGATTCCATTCCACAACATTTATTGAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
VI-13859	84 G A ---	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAACAAGTATATATTCAGGAAAGGACTCCTAGAACTTGAGCA ACA
VI-13536	29 T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAG[T/C]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
VI-13373	52 G A ---	---	---	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AAGTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCCAGAGCT
477b	61 A G ---	---	---	TGGTTTTTAATACCTCTTGTGGATAAAAAGGACATTGTTTTTCATTAGCTTGCTTCAAA[G/G]GAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
477a	32 A G A A G G	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAGAAA CAATG	TGGTTTTTAATACCTCTTGTGGATAAAAAGG[G/A]G/CATTGTTTTTCATTAGCTTGCTTCAAAAGAC AGAGAAATAAGATAAATTACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

14297	86	A T G	AATGTTGGGT AC TTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGAC TTTA TTTAGCATGCAATGCAATTTATCTTGGCAATAAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAG[A/T]JAAATGTTTCTGAAATGTGCACACTAGAATATATGCAGAAATCCTTT AAACAGTCGACT
12229	89	T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATTT GTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAATTT[G]ACCAAAAAATTAAGATTTTTTGGGACAATTCACATGTTT AAAAAT
13582	43	C A AGACTGGGA	TGCAATCTAG AAGACTGGGA	TCTGCGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAAATCTAACTGCGCAGAG AAATCAAGACCGATGGTGAAATCTGGGCGAGCTTCAAAATTTCTGCCCTCTAAACACATTTTCAC CCAAATTTTTCATTATTGCC
13857	28	A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAAATGT CTGCCCATTTTGTGTAGCTTTTCATACAGTACAGATTTTCATTGATGTCGCTCCCACATCTG
15809	77	T G TGTAAATGCC	TGGTTTCTGT TGTAAATGCC	TAAGTAGCTA ATTCAATGTTT GTAA	GTTTAAAGTTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[T/G]TTTACAAACATTGAATTAGTACCCTTAAGTATTGAAGAGCTTCCATT
15892	123	A T ---	---	---	TAAATCAGTCTGTGTCAAGAAAGAACAGGACTTGATCAAGCTTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAAGAA[A/T]JGGAATCA ACTCCACAGATCAACATGT
801b	81	T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TC TTTTATCCAAAGATGGGAAGCG[A/C]ATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTCTA GCTGCAGTAATAC[T/G]GCATCCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
301a	24	G A AATGGGAAGC	TTTATCCAAAG AATGGGAAGC	TCATTCAAGCC AATGAAATG	TC TTTTATCCAAAGATGGGAAGCG[A/C]ATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAATCTGCATCCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
13763	59	T C GCAGTGAT	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATTT[C]JAGGG GCAGGTGTGGGCAGGGTGGGGCTCTGAGCCGAGGACAAATGTCATGGCAGAGCTTCCAGAA
13578	48	T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTTT GTC	TTTTTTTTTGGTGAGTGTGTTCTTCAATAAAGAGCAGAAAGAAACCTT[A]AGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTACCCCAACATTGATATTTTGCCTTTTCCCGAGGGCAAAAAAGA GAGTCTCCCAAGAAACCTC
3789	62	G A AGGGAG	TTGGATGGCTG AGGGAG	CAGTGCCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGCTCCTCCTCTCTT GAGGTCCCT
3594	66	G A AGC	TTTAAACACA GATCACAAA	CCTTTGGCCA GTACTTTTT	AATAACAAGTTTAAAGTTTCAGCTGCAATGTTGGCAATGCAGGTTTTTAAACAGATCACAAGAAAGC[G/A]TGCACAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

NI-15625	40 C T	GTTCCTCCACCTACTCCCGCAGAAAAAGGCATATTCAA[C/T]TGTCCTACTAATAATTTTGAATAA CCTAACTCTCCCTTTGTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
NI-13367	84 C G A	CCACACTGAA GACTCACCAG	TCCCCACCCCA CCCT	GTCTCACITTCITGCTAGGCTGTAATTTTCAGTTTAAACAAGTTCTTATGTGATTTGTGGCCACACT GAAGACTCACAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
NI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCAAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGCCACCATCAGCAACCCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAAATATTTA ATATTAAAT	GATAGGAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAATATTAATATTGTCATGAGGTATGCACCT GCCCC
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAAC	CAGCTAGGAT ATGAAGAGTA GTTTTT	GCATTAACATTTAAAAATTTCTGAGGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTCAC TTTTAAAAC[A/T]AAAAAACTACTCTCATATCCTAGCCTGATGACITTAAGTTACCCG
VI-14319	83 C T A	CAATCAATTT GCATTTTCCTA GAAAA	CAATCAATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
I-13528	80 A G AAA	CAATCAATTT GCATTTTCCTA GAAAA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAATCAATACATTTTGCAATTTTCCCTAAAA AAAGAAGACATTT[A/G]TTTCAGAGAAAACTGTGGTATCATGCAGGAAAAAGCAGAAAAAATT ACTTAACTGGCTTATCTTCACGGTAATCTATTCGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACTCGAATACTTTTTC[A/T]GAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
I-1909b	80 G A C	TTCTCACACT CTCTTCAAAC CTC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACTC[G/A]AATACTTTTTCAGAGATGCTAGTAGTACCCACTGCAACATCTCTCAA
323b	86 C A	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTATAAAGGGACAGAAAAATTAAG AATCAACATCATCTGGAC[C/A]ATGGGAACCTTGAAAAAGGCATGGCAGTGAGACCAGTAACATA
323a	78 T C A C A	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATCCAAATGTAGCAAAATCATTAAAAACAAATTATAAAGGGACAGAAAAATTAAG AATCAACATCATCTGGACCATGGAACTTGAAAAAGGCATGGCAGTGAGACCAGTAACATA
I89b	104 G A AAA	AGATAATGAA ACATCTGCGA AAA	GATGAGGTGAT TCCACACTT	AAAATTGACAAATCAACTAGCTTGCTTTTGTGCTTTTGGAAAGACTACCATTAATTCAAAATTTATATGT AATACACTCATCCAGATAATGAACATCTGCGAAAA[G/A]AAGTGTGGGAATCACCTCATCTGTGC

NI-15389a	33 GA TC	AATCAACTAG CTTGCTTTTGG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCTTTTGTCTG/GA/TTTGGAAAGACTACCATTTATTCAAAATTTAT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAAGAAGTGTGGAAATCACCTCATCTGTCG TGTAATCTGCTTACAGTCTTTGCAAAAGACAGACATATGTTTTGCATAAAGATATAAATGCTTCAT TTTAAACTAATTTAGTGTCTT/CJT/TAATATATGAACCTTTTGGTGAATTATGAACGTGTACCAAAC C
NI-15747	88 T C AGTGTT	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAGTTTCATA TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCGTTAAGTCTGGATATACCTGGCTTGCAC/C/TTGGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752b	117 CT ---	---	---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCGTTAAGTCTGGATATACCTGGCTTGCAC/C/TTGGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752a	106 T C AGTGCTGA	CCTTCTCGTTA AGTGCTGA	CCCTCCGTAAA AGGTGTCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCGTTAAGTCTGGATATACCTGGCTTGCAC/C/TTGGACACCTTTTACG GAGGGATTCCGGACAAC
NI-14339	102 T GTTAC	CCCAATCAAA CAGTACATGA	TCCAGATTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCAATCAATCAACAGTACATGATTAC/T/G/CGGTTTCCAGAAATCTGGATAC TGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAAATGGAACCTTCATGCAGCTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACCTGAA/C/TTGCTGTCTTATCTTTC CTGATTCT
NI-14061	68 CT ---	---	---	CCTTGACTATATTGTTTTCCAAAATAGGACTATGTGTAGAGAGAGCCCCCGTACATACCTTAT IC/T/AAACCATTTTATCCACCATTTGTAAAAATCTCATCTCTGGGTCTGGATACCTCAAAAACAGAT
NI-15719	69 A C CATTGAGC	ACCCTTTCATC CATTGAGC	TGACTCTGGC AAGAGTTTAA ATT	TTACAGTTGGATTAACACTACCACACTGAATATACTGAATTAACCTATTCAACCCCTTTCATCCATTCAG C/A/C/AAATTTAAACTCTTGCCAAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
-13810	106 T C AACTT	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAATCAACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTGCA GGTATTAAITGGTTCTCTAAATCGATACATCCAAAACCTT/C/JAGTTAGCAGCAAGCATCAGTTCTTC
'36a	27 GT CACA	ATTTTATTAC ATTAAACTTG	GTTCTTTGATA TGTGGCTTAGT TTT	GGATTTTATTACATTAACTTGACAC/G/TTAGCAAAAAAATCAAAACATAAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTTTCCATAAATA TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC/G/ATAGTGACACATAGCTGTCAACACACAGT
85d	72 GA ---	---	---	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACAAATGAAC TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC/C/CAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG
85c	56 A/C ---	---	---	

II-3785b	40 C G ---	---	---	TCAAACCTGCACACTATAAAAGTGCTTTAAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGCTAGTGACACATAGCTGTCAACACACAGTG
II-3785a	27 T C TGCTT	AAAACCTGCAC ACTATAAAAG	TGTTGTGACAG CTATGTGTGAC T	TCAAACCTGCACACTATAAAAGTGCTTT[C/JAAAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGCTAGTGACACATAGCTGTCAACACACAGTG
VI-13793	88 C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATATAGGCAAAATAAAAATAGTTTTTACCCCATTTGATACAAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCCATAAATCTATGACTTG
VI-13794	52 A G TTCTTTCTC	TTCTCACCCCT TTCTTTCTC	AGAATGGGCTC TTAACCTTGTA	TAGTCTCCTACAATTCCTTCAATCCAATTTCTTCTCACCCCTTTTCTTCTC[C/G]TACAAGGTTAAGA GCCCATCTTCAACAAACAAACAAACATAGAGCAAT
VI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGACACTTTGAACCATGTGTAGACTGC[A/G]GGCACTTTAGAAAGAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAAGGAAGGTAAGTCCCTGTTTGAGCCCGGGGCTGCTCATTTGTTA
II-13424	66 G A C	TGAGGTTTTTC ACCCTATTCTT	TTTTTCTCCCC AGGGTCTA	GTCCCTTGCACAAGTCTCCCAACTGGTTTGGAGTTTTCCCTTCTGAGGTTTTTTCACCCCTATTCTTC[C/G] TAGACCCCTGGGGAGAAACACATGTGTAAGTGCTCAGGACATGAGGCAGGCCGCTTCACAAGAT GCTGGCTAAGGGCTTC
I-14065	29 T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTGAGAGCAATTT[C/JGAGATCCAGATTCAGCTTGCTCATAAAAGAT TCAACTTCAAGTAGCACAATTTCTGTCTGCTTTTAACTCTGAACATCTTGAAGCAGCA
-13446	22 G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTTCACCTCATCA[C/G]CCTCTCTGATTTTGATCCCTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTTAGGGCCTAGTCTGTTTAGAAATCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAAT
-13725	56 A C TGGGTGOC	TGAGCACATA TGGGTGOC	CCTGCTGTCTC GGGC	TCACACAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/JGCCCGAG ACAGCAGGATAAGTTTCACAAAACCTGACCAGGCAGGTAGAAAGCAAGGCATGGTTACAGGATG CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCTGTAAACAA[C/J]ACTAATGGGTCTTTGAACAAATAGTTT TGA
202d	107 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCTGTAAACAA[C/J]ACTAATGGGTCTTTGAACAAATAGTTT TGA
02c	101 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTCTTTGAACAAATAGTTT TGA
32b	90 C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTCTTTGAACAAATAGTTT TGA

702a	48	AACAAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAACTGTAAACAACTAATGGGTCTTTGAACAAATAGTTT TGA
831b	113	T C ---	---	TTTTTTTTTATGGATGCACCTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT ACTTCCACTGTATCCTCCGGGTAAGTTTCCCTCTCTCTGTAGATGCTCCATGTTACAGTCAAC TATAAACATGGCTCA
831a	56	G C ---	---	TTTTTTTTTATGGATGCACCTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAAGGAGATTCACAT CATACTCCACTGTATCCTCCGGGTAAGTTTCCCTCTCTCTGTAGATGCTCCATGTTACAGTCAAC TATAAACATGGCTCA
-13806	62	G A ---	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACCTAGGCCTCAGGT[G/A]C CCATTAGCATGCTGTGAATGCAAAAGGAAAAGCTTAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
-14372	86	A G ---	---	CACATTTTCAGCAACAAATCGAGGTGCAAAACAGGGTTTATTTACATTATATTAACGGATTT TTTGCAATAAATAGGGA[A/G]TCTCTTTAAATAACCATCTCCTCACTTCATGGCCAGT AGGCTGTTTTTGGGCTGAGGACCCCAACATGACAACGTAAAGACTGTAAACCATGGTGTGAGTT ATGAGCTAGGAACCTGGACGAAACCA[A/G]CACATATACAATCATCTCCACCTCCCAACGCCCTTT ACTTTCACAGCCTCTGCA
14078	61	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACATGGTGATCAAAAGAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAAGGACTTTAGATGGTCACG
14083	47	AGACTTGAGA GCTTAAACA ACACT	GCCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACAACACT[C/T]ATTTGTTATTTTCACAG CTCAGTAGTTTAGAGGTCCAGTAGGCTTGGCTGAGTTGTTTGGTTAAGGTCTTACAAGGCCAA
4085	31	A G AAAAAA	CAGTCATGTT ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAGAAAGAAAAAC[A/G]TAACCTAGCACGTGAACATGACTGCATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAAGTGAAGTGAACAAAAATAGCATGTTGATTAAAGTGAAA TAACAGAACAGGAGGCCCTT
2169	121	AATAAACTT CCTATTTTCTT TTGCTT	GGTCTCTGAGG TGAAAGAAAA A	GTCAAAGGTGGCAAAATTTATTTCCACTTATCAAGAACTTACAAAATATTTTGTTCATTTCTAAA TTTTACCTTTATTGCTAAGTTATAAAATAAACTTCTATTTCTTTTGTCTT[G/C]TTTCTTTTCA CCTCAGAACCCCTTA
705	50	GGAGGGAGAT TTTAGACTGA GATC	AGCTGTAGTCG TCAATACTCT AGAA	TTGTTTTTATTTGGGAGAAATGAAGGAGGAGGAGATTTTAGACTGAATC[A/G]TTCTAGAGTATTT GACGACTACAGCTCTCTCTTTGTACTACGGAGACCTGCTTATAGCCCCCAACAGGAAATCTCTCA TCTGCGGTGOCAGACAG

WI-14379	102	C T	TCTATTAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA	TTTATGCTGTTGTTTCTACTGGTCGGTCTCGCTCACTAATATCAATCCTAGTATGATTTTCTTT TACTTGTCCTATTACAGGGTTATGTACACCC[C/T]TGTCACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCACCATTAACAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGCCCGGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	---	---	ACCGCAGAGCTGCTGTATTTAA[A/A]GJACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACCACCCC TGAAACTGAAACGTATTTCTCTCA[A/C]ACACCCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGCGAAAAGGAAGTTTCAGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT GGTT
WI-15937	24	A G A	CTGTATTTAA A	GCAGAGATCCA GACGCTTGT	ATGTTTTATGATCAATTCCAAACATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-15944	24	A C A	AAACTGAAAC GTATTTCTCTCC	GGCCTTTAAGT TTCTACGGTG	GACAAAGAGGCAGTTCTGTAGTTCAGCAGGGCCAGCAGGATTATCAGAACGGGTGGTTGACCT GCATAGATTTTTCAGCAGT[C/T]GTGGCCATGCCATTCCTGTAAAGTGAAATTAATGAACA GTTTATTTCTCACAGTCTGGAGGTTAGAACTGAGATGAGGATATCACAGCATGGTTAGGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGTCTTCACAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGGT
WI-14124	92	A G	---	---	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAAATATTGTTTCTTATGATTGTTTCAATG
WI-14125	88	C T	GGTTGACCTG CATAGATTTT	GGATGGCATG GCAC	GGCAGGTTTATTCATAATTTTCAAACCTTGGAAAGCAACCAAGATGTCTTCAGTAGTAGTATATTCA GACAATC[G/A]AATATTACTTAGCATAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-14136	120	G A	GCTTCTCACC ATGCTCTCACA	CTGTCTGTG TCTTTGGGC	TTTTTAAGAGTGCTCTCACATCATTTATATTGTATTGCACACAACTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-14138	23	C T	TGTTGGCACCA GAAAAGCT	GTGACATAACA TAGAACA	TTTTTAAGAGTGCTCTCACATCATTTATATTGTATTGCACACAACTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-13551	74	G A	TCCTCAGTAG TAGTATATTCA GACAATC	GCTCATTTCTT TTAGTGCTAAG TAATATT	TTTTTAAGAGTGCTCTCACATCATTTATATTGTATTGCACACAACTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
953b	59	C T	---	---	TTTTTAAGAGTGCTCTCACATCATTTATATTGTATTGCACACAACTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
953a	26	T G A T	TTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTG	TTTTTAAGAGTGCTCTCACATCATTTATATTGTATTGCACACAACTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGAGATAGAAGCCTTCTTCAGAATCA CCTCCC

VI-14631	82	G A ---	---		TGAATTCATGGACAGTTTTGCCCTCTGTTTGTAGTGAACCCCTCACAAGCACTCTGCATAGTCGCGCTTT CTGTCTTCTTTAAAC[G/A]TGCCTGGTTCCTCTGCCAACTTTTAGGATTGGCCTCCTCAGGGCCTT GTCTGA
VI-6053	24	A G ---	---		ATCACCAACCGTGTCTAAGAACAAC[G/A]TCTTCATGTCCAACATCATCCCGGGACITTTGTCAACTG CAGTACACTTCTGTCATTGAACCTGGCTTCTCGGAGGGAAGCCTCCTAGAGGCCAGGTAAGGGGGTGC AGCAGTGAGGGGTATATCTGGGTGGCCAGTTGGAAACACGGAG
VI-15964	99	T A CTGGAGGTA	GACTTCTCCAC CCTCTTGC		CAGAAACCTCTTCTGTGTAATTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGTCCCTGGAGGT[A/T]A[GCAAGAGGGTGGAGAAGTCTTGGCAAG CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAAAATACCCATCAG AGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAG CCT
VI-12075	103	G A GGCAC	CCCTTCTTTTC TCITCCTTC		TAATTTAAAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTTCTAGAAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCATTCGAGGAGGAACAG CACAATAGTGAAATTATCTGAGCAAGAAATCATCTCAATTTAAATTTG[C/G]AAATAAGTCAGAA AAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAATTTTCACAGGTAAACCACTGTTA AATGTGGACTTTCAACAAGGGTTTAAACTAATCTAATACAACCTCTACAACACATTCAGAGCAT TATAACAAGAATTATTTACAGGCAGCTAATGTATTAAAT[A/A]AACCATGAAAAGAAAAAAGCTTG ATCTAGATGTCAGCAAAATGGGCTGAGACTG[C/T]TGCTGGTAGATGCAGTGTGTGATGTTTCTAC TCTATTACAAAAATTAAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATACACAGTC
13967	103	A C AAATAAAAA	TTGTGTTTCA TCTCCTAAAAG TG		AATTTAATAGCAGCTGTGTGTGATTTTAAAGAACAAGATAAAATATGTCAATTCAGCAGTCATTT AAAAATAAAAGACTACAGATACAAGGAAATAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA TTAATATTCAGCAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAA GTAACAAATGAGTTTTACACAATTAAATATTAAACACATACTTATGGATTGTTGAATGA TTTTGTGTTAAGAACAGCATTTTGAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGC
4408	60	T A G	CAITGAGATAA AGCACACTTAT CAC		TTAGAAAACTGATAAAAGCAACACAACTTTTGGGAAAGCACCATGGCAGCTCCTTTGTGCTA[C/T] GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA ACATGGCAGATACAGAGCTG[C/G]ATCTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGAGCGTTGAAGGGTGACCAGC ACATTTGCACATGCAAAA
3683	47	C G ---	---		
35	22	G A ---	---		

WI-16002	59 T	GATAACATAA AATGATCATG CAGAAATTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGCT GTGGAAATTTTAAAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAAGTCAAGTCATCA[A/G]TTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAAACCA TGAGTTACAACAATGAGCAACAAGTTAGAAAAATGGTTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGCAGTGTGGACGGGAGGATTGCAACAGAGTTTCATACTG CAA	
WI-15361b	101 A G A	CCCACTTGAAC TCAAGTCATC A	AAACTAAAC CTTTGTGCCTA AAA	TCCACACTGC OCC	TCCCTAACATTTATTCAGGTGGTGACTAGGAGGTTGAGGTGTAGATAT[A/T]CTTCCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCGTCTTGTTTATCAGCTGAGAAAGGCAGTCTCGCCATC TTAAGACCTGCCCTCC TTCCATTCAATTATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAAGGAAATTTTGGC CCAGAAACCATGAGATTTGGTCAGAAAAAGGCACACGGGAA[G/A]GGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC ACACAATATAATTCATTT[C/C]GAGTGATTAAAACTATTTGTTGTTAGAACCAACAAAACTAC AAGAAAAATTTTCAAAACCTTTTTTTCAGGCTGA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	GCTCCACGAGA AGAGAGGAA	CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCCACCACACTACCCTGTT[A/AAAACTCTTAAC ATTGTGATGCCCTGCTGCATCAATTTTAGAAAAACAAGAAAAACACAACACTGAAGGCCCATGTA AGTTAAAAAAATCGAGTCAGCATTTTATTT[A/AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCGTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-13805a	112 G A G G G A A	AAAGGCACAC	CTCAGCCTGCC TTGACC	CTCAGCCTGCC TTGACC	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12340	18 T C ---	---	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-14808	52 T A C T A C C C T G T	ACCCACCACA CTAACCCTGT	GAGGCATCACA ATGTTAAGATT TT	GAGGCATCACA ATGTTAAGATT TT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-14816	29 A T ---	---	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-142c	71 G T ---	---	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-42b	70 G T ---	---	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-2a	45 C T T T T A A A	GCTATTAGGC AAACTGAACA	TCTAGAGCCCT CACATGGAT	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATCATTGTTAGGTGATTGATACAAATACGATCCATAA CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC AT[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-173	57 C T C A A A A A	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT	CCACCTCTAGA ATGTATGCTCT	CACCTAAATCATCTAGAAACTGGGGATACAGCAGTAAAGAAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

'I-16083	89 C T	ATGTTTAAACA CAACATATC AAGGAT	TGAAAAGATT CCAGCC	GCATCTTTATTACCACAGAACTCATTTATGTCTTAATCATTTGTTAATAATAAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATCTATAGAAAAGCACTAACCATC CATTAAAGCAG
'I-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCGTGTCTGGAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGGTGATTTGGGAGCACGAGGGAGACAA TCAATACTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACA[T/C]CTCTAAATCATCCTCTA GATCAGGGAGTCATAGGACCAATTAAGGCTCATTACACACAGTACTTTATGGAAAGGATT
'I-14946	47 T C	---	---	ACATTAACACAGCACAAATTAAGGGTCCCAACGAGTTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A]GTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC ACATTAACACAGCACAAATTAAGGGTCCCAAC[C/T]GAGGTTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCATCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
5987b	80 A G	---	---	GAATAAAGTCTTATTGCCGTTCTTCAGGGAACAGGGAACTGCTAACTTGTCAAG[T/C]TCCAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTAGGCTTGCTGTCCCTCCAGCTGA
5987a	32 C T	CACAATTAA GGGTCCCAA	GGAAGGCACTA CCAACTC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTCTGACATTCCTGTTATCAACTCCTCTGAAAATC GTGATTGATCTGTAATATTGGGATTATTTATTCACACTCTAAAATTCGAAGATGAAAATAATTTATCT CTTCTTTTCAAGGG[A/G]AAAAACCCCAATGAATGCATTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAATTCAAAGGA
'I-14948	56 T C G	CTAACTTGTC GA	GATGATCTTAC ATCAGTTGTTG	TATTTTTTAATTGGTGTGTTGCTTCGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGCATAGTGCCACAAAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
-16100	52 A G	CAAAAAGCTA TTTCTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TAATTGATTCAGTGGTGTATTGGAATTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAAT AAGAGGAAAAAAGAAACAAAGTGGCTCTCGCATCAACGACCTGATCTGTACACAGGAAGTTTGTGA GAGCTCACAAA
14958	83 A G	AATAATTTAT CTCTTTCTTTT CAAGGG	AATGCATTGAT TTGGTTTTT	TGATTACATTTTTAAATCATGCCTACAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCACTGATCGGAAAGAAACGTA AAATCTCTTCTTTACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAATGCCCTTCTTGA TTTCCCT[A/T]TCAGTTTAGGCCTCAAATGGCTCTCCTCAAGGCTGGACCTCAAAGGCCACCT
14976	35 C T	GTTGATTTGCT TCGTTCAAAG AGC	CTTCCATTCTA AGC	TCAAACTAAAT CTTCCATTCTA AGC
4981	31 G T T	TCAGTGGTGT TATTGGATTT	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGAATTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAAT AAGAGGAAAAAAGAAACAAAGTGGCTCTCGCATCAACGACCTGATCTGTACACAGGAAGTTTGTGA GAGCTCACAAA
1992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCCT	TGATTACATTTTTAAATCATGCCTACAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCACTGATCGGAAAGAAACGTA AAATCTCTTCTTTACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAAATGCCCTTCTTGA TTTCCCT[A/T]TCAGTTTAGGCCTCAAATGGCTCTCCTCAAGGCTGGACCTCAAAGGCCACCT
002	72 T A	---	---	TCAAGCCAAATATCTGCAACAATAACATGTAATTGAAAGGTATAGAAAATAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAAATAATCCACCT
200	90 G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTAATTGAAAGGTATAGAAAATAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAAATAATCCACCT

11-12323	68	GA	CACAATACCTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTTGTGATGTTGGTTAAATCTTCTTTTTTATACACAATACCTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCCAGTGCACACAGAGGACTCACACCTGTGCATAGACAGCACC
11-14683	91	A	AAGGACGAT TTAGTATCTAA TAAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA/VJCAAAAAAACACTGGGACATGCCCTGAAATTGCAAGT TGGAGTTCGTAAGAATCTAC
11-13470	100	CA	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTTGTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCTTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCOCTTC
11-14712	38	T	TGAATGCTTC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAGTCAAAATCA/T/AJCTCACAATACCATATACAACATACT TTCAATCACAACCTCAATATAAAATAACCTACAAAATCACATTGC
-13712	40	A	TTTACTTTGTT GTCATTTTAT CTCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTTACTTTTGTGTCATTTTATTCTATTG/A/CJATTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTGTTAAATTTATGCAT
16163	35	CT	TCGTGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACCTTAC AA	TCCTAAGATTTTACTCTGCTGATGCAATGAAATAA/C/TJATTGTAAGTTAATGTAAATGGCAGCATT GCCCCAAGTTAAGAGGACTATTTCTTTAAACAAAGACAGTGTCTGACATTTATTTTCAGGT
13453	88	T	AATGCACAAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTTGCATTTGAGTGCTTTTATTATATTGGGAATTCAGTGTATTAACATTTGTACAAAT GCACAAATCTTGCTCTCTTC/T/AJGTAGAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCT
3167	58	T	CGCACTCTAA ATTAGAGATA GATTTT	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTTC/CJATCTT ATTCACCACGAGCACACCCACGCACAGTAGAACAGTTCCACACCTGATAAATGACACAAGATG
482	17	GA	---	---	GCAGAACCAATTAA/G/AJAATCTGCAAGTTTTCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTTGATGTGACAGTCACTGGT
269	81	T	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATTTCCAGTATCATGTAC GCACTAAAAAAATTC/GTGTGCTTGTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
56	97	A	TGAAGATTAA CCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTTGTGTATCCCAACAAGTATACAGAACTCTATAAAACCAACCCACCTTCAATA TTACACTAATGAAGATTACCCAGAGTCGC/A/CJCTCTTCAAAATGCACACAATTAAGACG
12	59	GT	GCAGCAAGAT TACATCAGTA ATGT	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATATAATACAGCTTTTTTCATTGAAGCTTTTG/TJACCTT TACTATACTTAGGCTATTGGAGTGTCCCCAC

WI-15100	74	G A ---			TCTTATTCACAGCCAAAGAAATACCCAAATTTCCAAATTAATTTCCAAATAAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTTCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT
VI-14492	92	A T AATTACT		GTCACCATGTT ATATTTCTTT TAAGAC	TGGTACAGAATGTTTAATTACAGCGGGCAGTGATTCCAGTTAAATAAATTTAAAAACCTTTATTTT CCCAATATATAAATTAATAATTAATTAATTAAGAAAAATATAACATGGTGACAGCTTT
II-2002c	89	T C ---		---	TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCATGGTGACAGCTTT ACGAGACACAACCTCTCCCCAC[T/C]GCTCTAGAGTGGGACAAAAGTGGGGTGAGAC
I-002b	68	G A ---		---	TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCATGGTGACAGCTTT AC[G/A]GAGACACAACCTCTCCCCAC[T/C]GCTCTAGAGTGGGACAAAAGTGGGGTGAGAC
102a	30	C G GGACACAA	TCGGAATCCA	TGGTTTTGGG TGTTTTCTT	TCTTTAATTTTATCGGAATCCAGGACACAAC[C/G]AAGAAAAACCCCAAAACCATGGTGACAGCTTT AAGACGAGACACAACCTCTCCCCAC[T/C]GCTCTAGAGTGGGACAAAAGTGGGGTGAGAC
15116	96	C T GTTGACGTAA	GGGAGOCCTA ATGACA	CCTGAATATGC AATTATTTATT ATGACA	TTTTCATTTATTTCCAGAAAAAATCACAATTTTCAGTAACAACCTTACATATAGAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAAATAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
2578	37	C T AATGGGAA	GGCCTAAAGG	TCAAGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGGCCTAAAGGAATGGGA[C/T]GTGTTGGTGGTGCCTGATACCTTGGT GCTTGTGTGCTGGAGCAGAAAGTCTCTCTGCTCAGGGGCGTCACATATTTAACTGCACATAAT TTGGGCAACTGTCACTC
153	40	A G GCATTGCA	CCCTTATGTTG	AACCTCAGATA AGTGCAGTGT T	ATTCACGTTGGCCAAGATCTCCCTTATGTTGGCATTGCA/GAAGACACTGCACCTTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCTCTAA
215	84	G C TCAAATGGG	TGGCTTTAGAA	CCAACAGGGGA AAAAGTCA	CCTTTGCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAATGGG[C/T]GACTTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGCA
25	80	C T C	CTTGAGGACCT	TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAGGCGATCATTTGGATGAATGATTATGTGTCAGGACCTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATTCGAAGTTGGAGATATGCTAAAA
32	51	G A ---		---	AATTTGCTAGTGCAAATGGACCCAGAAATTTGGAAGGGCTATGTAACACACAC[G/A]TATGCACACCCAC AGCCATGTCAGTGCACAGATCCTCTGTGATTCAGCTTTCTTAAAAACACATCAAAGGCTGCA
3	55	C T TAGGATG	TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAAACAGAC	TGACTGTATACCAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAAAACAGAGATAAACACAAT

-68-

11-14528	62 T G	TTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA TATTTCTTTCCGTTTCGGATGCAAAACAAAAATTTTAAAGAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTCT/CAAAGACTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
11-15347	74 C T	GACTTCAAAG GAAAAGAACA TAAAT	TCAC TCCCCCA AGTCTTTG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTCATATACAGATCA TTTATTGGCTGTCTGTATAACAATGTGGTGAACAC[G/AJCTTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGACTGCAAGACCAGTGTGAGGCACATAGGCTGATTATCAGTGG AGAAATTTTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTATACACATTTCCCATCTGTCTTGCA[G/A]GGAGGGATCTTGGTCGGCTTAACA CCAGCTGGAGGTGGAATAAATGCGGCAACACAGAAAAACACAGCTACACAGGCCTGCATT TGGCTTA[T/C]GTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAATGTCT AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCATAGGCACATCAGAGTAAATACTG TTTGGTAAACTTGTTCAGTTT/CJAAATATGTATGTCCGTGCATGTCAATGATTAAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACAACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATTTTAAATGCCGAGCCGACACCCACA AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAATGCATAGGCACATCAGAGTAAATACTG TTTGGTAAACTTGTTCAGTTT/CJAAATATGTATGTCCGTGCATGTCAATGATTAAATATCCTTCT TACCACAGTCACTTAAAGAACCAAGCTTAGGACTAGGACACAACTGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATTTTAAATGCCGAGCCGACACCCACA CACAACATTCAGAAATTTTCTGCAATGTCTCTCTGTATGTCTAAAGATTGAGCTTTGACTAT ACGATTTCCACACTGAACGATTCATAAGGTTTCTCC[C/C]A/JAGTATGATTCTCTGATGATTAAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTCTCCAGTGTGGAC TCTCTGGTTGCACAAGAATGGAATCGGCTGATGCTTCCACACT
11-14546	95 C A	CCAAATTTCTAG TGATAGTAGA GGACTCA	AAGTGCACGT GCAGG	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
11-15353	37 G A	---	---	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
-14580	100 G A	CATCCCATCT GTCITGCA	CCGACCAAGAT COCTOC	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
-8540	73 T C	GGCCTGCATTT GGCTTA	GCCTTCTTTT TCAGGCAC	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
1039b	97 T C	---	---	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
39a	87 T C	---	---	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
4	107 C A	---	---	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
32	32 G A	GGGAACATCA ATGCAACAAG T	TTTGGGCTTG AGTTTACAAAT	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG
87	7 T A	---	---	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA TATTAGATAAAACCTTTGTTCCCGATTTCAGGATGTTTAAATTTGCTTCTCTTAACTCTGTGACTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG

-6192	91 A	GAT	GACTGCTAAG GATTTAAATTTG	TGAAGTGTTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCAACATGATTGGCAGTTGGCATATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTTAAATTTGGAT/GJATTTTAATACTTAGCCATCTAACACTTCAAGCATAAC
-6194	105 T A	GAAA	CACATGGCAA TGATAATAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGTCCTCACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACCTT GTCACCAAGAAGTCAATGCGCAATGATAATAAAGAA/TI/ATGCGAGACTACACTCTGAGGATAG AGCTTAAAGAGTAAACAATGGAATTTGGAAAAATAGGAGTAAA
-6213	164 C T	---	---	---	CATATGCTGCTTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTCTAACCACTCTACAGAATGTTAGTATGTATTGCTATTACATGTTT ACTTTTGATATTGCTCATTAATACTATG/TI/ATATAATAATGTAGAATACAGTAAGTAGGTGATCC TGCAATTCAGGTAAAGCGTAGGTGGAATCCAGATTTCTCTTGAGGAAAA
-6217	131 C T	---	---	---	CGGTTAAGAAATACCTTTAAATTTAGTAAATAAGCTCAAGGAGGTGGGCTGTCATCTGTGGTG TCAGTCTCTTGCCCTGGCTGGCTGTCAGTGCCTCCAGGCCCTTGACAAGCAGCTCATTTCAAG/C/T GGCCCAACCATGGCCCTAGGTCGTCAACAAGTCCAGCAGCAATCATGGCTTCGTATATCTGATCC AC
-6238	175 GA	---	---	---	ATAGCTTTTATTGTCAACGAAGGCTACACGGGATCATTCTGGTTTTGTTTTATGCTTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTACAGCCTGTTGGTATTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAAT/GJ/ATCCAGACTTCAGGAAAAATGATT TCCACATGTTAAGGCCAGAGCTCCAGTGTGGTATCCAGAACGCTTG
-6272	86 C T	TAA	GCATTTATTCA GGGAAACTT	CTGTTTTTGGGA GAAGACAAAG AA	CTTGATTTAATCAGGGCTTTGGGTCATAGGGGATTAGTCACTGTACAGTCATAATAATGCATTTA TTCAGGGAAAACITTAAT/C/TTCTTTGTCTTCCAAAAACAGCTGTGGAACACCTCAAATTA GGGATGTTTCATCTAAACACCTTTACTGAAACTTGATTCCTTGGCCAGAGGAGTCTTACTGTAG CAGAGGACTTAATGCAATGCCTATTCGGGCAATAATGAATCTTGATGCATTCATACAGGCAAGAA TCCCAGCATCCCAGAGAAGCTCTGTCTG/CJ/ATGCAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGCACTTCTAGTCTCGCTCGCTTCGATTTCCCTGCCAGCAGTCTCTCTCTCTCTCTCTGCCC TCTG
03	96 GA	CTCTGCTGC	CCCAGAGAAG CTCTGCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGATGATTCTAATTATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGATGCATCTGCTGCAATCAATCACTGTAATGTCCATTGTCCA CTTCCCTTACATCTTTTGGGGGA
5b	193 C T	---	---	---	ATGCTTTTGATGATTCTAATTATTGCCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGATGCATCTGCTGCAATCAATCACTGTAATGTCCATTGTCCA CTTCCCTTACATCTTTTGGGGGA
5c	187 T C	---	---	---	AACAGTCCCTTTTCAAGCCAGCGTGTGATGCATCTGCTGGTAAAAAGTGGGTGCCATACA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGT/CJ/AGTGTCTCTGCTT CTTCCCTTACATCTTTTGGGGGA

-6375	28 A GAA	GGTTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTCATATGGAATCAATAGAGJATCTTTTACAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACATGTGCTTATCAGCTCCCTCCACCCCTATATTTAAJAGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACJATJATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
I-6409a	73 A T ---		---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTTGACGAGATTTTATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTGJGJATATCAACCTTCCCTAAGCATCTGTCTGGTCCG
-6523	165 G T C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	CAGC TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCTGGTAGTCTCTCTTTTCACACAACCTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCACAACAACAGCAAGCTAAACCTCTGAGAGAAAACJGJCTG
3554	195 C G ---		---	ACTTTCAGAAAGCATAAAGCTGAGAAAAA ATTGTAATTAATAATTTACATGGCCCTATTTAATTAAGGACATTTGTAAATGTTCCACTTTGTTTTAA JCTJAAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGGCG
358b	68 C T ---		---	ATTGTAATTAATAATTTACATGGCCCTATTTAATTAAGGACATTTGJCTGTAATGTTTCCACTTTGTTTT AAACAAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAGTTTGAAAAATGGGCG
58a	42 G C ---		---	AACCAACAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCTATJTCJAGCAATGGATGCTGTGAGAACATAGTCCCAATAAATTTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAACAGGAGCTCACAGCGGATGTAAAGATTAATGGAAGAT ATCGTGAGCCAAAAC
9	75 T C G T C A T A	TCTTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAATCAAAATCAATCAAACTCCAGCTGTTCTCTGCTTT TTACTTAGCAAGGAAACCTTGTAGTAATGCTACTTGACAAGAAAGATCATTTCTCAAGCACAJ T/CJACCCAAACTTGAAGGTGATTGAACCCAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATTTTGTATTTGCTGCTT
134 T C ---			---	TGCTAAACACCAACCATTTAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGCCTJGGCTAATACACTGCAATATTTTA TGTTAGCAAATTATAGCTGGTCTGTGTATAACCAAGAGCGGTATCTGG
106 C T	CAGACTCTGG AGCCACAGC	TGACAGTGTAT TAGCC	ACATAAAATA TTGACAGTGTAT	

VI-6690a	28 T C	AAACACCACC ATTATTAAGG CAGAG	GCTGTGTTGG TAGTTTTTCCT	TGCTAAACACCACCATTATTAAGGAGAGTTCJACTAGGAAAAAACTACCAACACAGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGCACAGACTCTGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTTAGCAAATTATAGCTGGTCTGTGTATAACCAGAAGCGGTATCTGG
NI-6770	53 A G	CAAAACCCAA AACATCACA	GCTTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA[A/G]AATTATTTCAT ACTATTATACACTCCAAAGCAAAATACTTCAACTGCAATCC
VI-6686	151 A G A	GCATCTTCCA AAAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTTCAGCAAAATCAGCTAGCATAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTTAGATGAATTCACATTTAAACATGGTAACTCCAAGCATTCT TCCAAACAAAGAAT[A/G]AACATTGGAATAGTCACTTACAAGGAC
I-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGATGG[C/A]CTTCTCTCCAGCTTTTGTGAACAAAAAC AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTTTCAGGTACAAGGTCTC
6844	225 T C	---	---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGCCATCATTAAAAACAAAGGGTATTTCTCCTTG GTATTTTCAAATGATGCATTATACAATAACGAAGTTAGAACTTAAATGCACCTGATTAATTATG TAACTGGTAATTTGTTTAAAGCATATAATTTGGTCTCTTCTTCATAAAATGGAAATTTTAAA TATTTCTCTGATAGCTTGAGGTT[C/A]TCAATTAAGTAGTGCAAGGTG
824	112 A G	---	---	CGGTTTGTACACTTAAATGGGTTTTTTTTAAGGGATTTTTTTCAGGCTTGTGTCAGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGTACAGAGTGTGCCAA[A/G]CACCTTAGAAAAATACAT GACACGGAGAAAAATGCGCTCTTGCTCTTGAAGAGCTTACAGTCTAGGGATTGACAACCTCACAGT CITTAGGAACIGGGCAAGTAAGGCAATTTCTATCCCTAGAGCTATTGTG
389	139 T C AATTC	GAANAATGAG ATGCAGTTAA TCT	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCCAACATGGAAGTGTCAAGAAAAACATTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAGGAGTTACATATTAGTTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC[C/J]AGAATAATTAAAGCCACAAAGTGAAACTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
11	216 T C	---	---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAAATATCTGATGAACCTGAACTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGAAGAGAGAAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCTTCCCAAGGAATGTGTTCTAATTTGGTTTCAAAGCACACTGGTTCC CAGTTTTACCACITTT[C/J]CATGACATTTGGACAATAGTACTACTTTTCTAC
3	112 G C	---	---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGACAGCCCTGTTCTATATGAAGACAAAAC AGGTGGCCATACTTGGGTGGAGGGATACCGCTGCTATTCACAGAT[C/J]AAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
74	CT	---	---	AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCAGCT ACAGCCTTC/JGGTGCATCTTAACCCCTCTCCTTTT

VI-9617	37 G T ---			TGCTCTTTTATTTCACGTTTACAAACACACGCCGTG[G/T]GGCACAGTCTACCAAAGTGGCCGAG CGCCACGCTTGGCCGGAAGGTCTCATTTCTGCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTTGCACGATGCAGCTTGCACTGGGTCCAGCCGGGTGCTGTG
II-9657	121 T G ---			AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGGTGAAGTATAGTACCATCCACTAT CATGAATTTTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAG[T/G]ATAATTCCTT TGTATTAATAAATGTTTATAATGTTTATGAAGCTCATTACATTATCTTTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTTGAGG
119b	114 G C GCTGGGA	CCTCCCAAGTA	AAAAATTAAAC CAGGTGTGGTG T	CAGGGCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGACTACAGGCATG[T/G]CACACCACACCTGGTTAA TTTTTTAATTTTTGTAAAGATAGGCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAAC CAGGGCTTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[T/G]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGACTACAGGCATGTGACACCACACCTGGTTA ATTTTTTAAATTTTTGTAAAGATAGGCTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAA C
19a	51 C G ---			ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGCAAAAATATTTTAAATTGAGGGAATAGGCCAAT TT
3112	71 C T AGCTTTTT	TCATAAAGAC TACAGACTTA	TTAGAAATTTT GTGTATTATAT GGAAAAAG	TGTTAACATTTTTATTGGTACGTGCTCTCAGTACAA[C/A]AACAGCATCAGTAGTGTACACTTTGAT AAAAAGGAATTTTTAGCTTAGTAGAAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAACTGTTTGTGTGACCCTTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
988	36 C/A CTCAGTACAA	TGGTACGTGCT CTACTGATGCT GTTT	CAAAGTGTA CTACTGATGCT GTTT	TGCTATTTCATGACAGACAGTGTGACACAATATTTCTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTTAAACCCTAATAGTGGAACCCTGAGACTTTA[G/A]ATCTGCAAGGGGTTTAAATAT GCAAATATCACATATATTTCCATTTTAAACACCATATTTAAGTTTCCATTTCTTAAAGAAAATGA TAAAAAATGTTTTCCCAATAT
108	G/A CTTT	CTAATAGTGG AACCCTGAGA CTTT	CATTATTAAAC CCCTTTCAGA	TGTATAAAAAATCCAACTTGTTCACAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCC[A/G]TACAAAAAACAAGCATTTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCGGATGAGGCAAGCA AGTTGTGTC
7	87 A/G AAAGTCCA	CCATATACAT ATATCAAGGT ATGCTGTTTTT	GCCATAGGAA ATGCTGTTTTT	

12611b	50 GC ---	---	GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCGTGTC[G/C]TCTCCTGGCCTCTAG TCCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTATTACCA
12611	34 TC ---	---	GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTT[C/C]CTCAGGTTGCCGTCTCCTGGCCTCTAG TCCTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTGTCTATACCT GCCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTATTACCA
1172b	179 C T A	TGAAGAAATG GCTGATACCA	GTAAAGCTGTGGTTAAACTAGGCAATTGGTTAAATCAATTTAAACACAGGCCCTAGAACAGTG ACACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/C]TGCAGTGAAAAATGCA CATGATGAGCCTGGAAACATGTTGT
172a	17 C A ---	---	TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAATCAATTTAAACACAGGCCCTAGAACAGTG GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTGAGTGAAAAATGCA CATGATGAGCCTGGAAACATGTTGT
77	35 G C A	GCAGATTGGA AGTGTGAAA	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAGAGTCTAAATATTGCA AAATGTAAGTGTGCCCTCAACTGTTCTTTACCCACTTAATCTGCAATTTTGAAAACTAGATTGAAT TCCTTTGCAAAACCTTGCATCATGGATACCCGAGTTAAACCGTTAATTAAGACATTAAACATGG CCTGGTG
1b	141 G A ---	---	TCCATGGTTGGTTGCTACTGACTTTGTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTCTTTTCAATTTTCTT TCAC[G/A]TTATCCCTCACCTGAACGCCCTTCTCCTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
a 126 T C A	GGCTCTTTATT CTCCTTCTTTG	CGTTCAGGGTG AGGGAATAA	TCCATGGTTGGTTGCTACTGACTTTGTAGCCTTACTGCCACTATGCATTGGAACATTCCTCATATTC CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTCTTTTCAATTTTCTT CTTTCAGGTTATCCCTCACCTGAACGCCCTTCTCCTCGTAGTGACATTTTAAATCCACTTTTACA CATTCGGACC
114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCCTT TCCAGCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACACAGAAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAATGCAAGGCTGACAAATTTGGGCTTGATT

NI-478	46	CT	GCATGCTGTG TTACTCTATTT TGTTTC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTGTTCTC/TJAGCCACCTGTGGCATTTT CAAAATATGATAATCTCTGCCACCATCTGCTTTAAACACAAATAGAACTCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
NI-533	29	T	ATCACAGCAG AGTACCTTTCT	CCITCCAACCT CTACACAATCT	AGCCATCACAGCAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTTGGTATATGACCCTGTGTCCAGTTAATCCA
II-601b	112	T	A	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCATTGACTCTCTAACTGAGTACT/JCAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
-601a	74	CT	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGATGATCAATTTCAAATAAAGATGG TAGTGAGCT/JGAACAGAGAGGTTTCATTGACTCTCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
863	107	A	CTCCTTCACAA GCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAACAGACACCTCGGCTTCTCACCAGTCCACATGGTGCCAAACAATCCCACATTCTCT ACATCTCTCCCACTGGGCTGCCCTCTTCAACCTCACCA/JGACTTGGCTTACCGGGAAGCATAAA GCCAAGCAITTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
19	36	G	ACTGCTTGCTT GTTGATTTAAT	TTATTCTAATC CCACATGACAG	ACTCACTGCTTGGCTTGTGATTATCAACCTAGCC/GJGCTGTCTGTGGGATTAGAATAAAATA AACACAAAATGAANAACACACGATTGCTAACAAGCAGATCTTTTCAAGGCACACGTAAAGAT AATAACTTCAA
1	37	A	T	---	TGCATTCAATTATGCACCAATAATAACTTCTGTACAT/JATTCATTATGTTTCTATTATCACAAAAT TATGAGTGAGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAATATCT TTCCCAAGTCACAAAGTTAGTGACAGAGCCGGATTGCAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACTGACTCTCTTTTCTCCTTTGAAAACAAGGC
1	70	G	CAGTATCTGA AGTTTTGTCT	AGGAACACCTA CAAAATGACTT	CTTCTGACCTGTTTGCAGTGGATACTGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTGTCTCC A/GC/JAGAAGTCAITTTGTAGGTGTTCTGGGCTTTTGTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGCTTGCAGAGCAITTTATCAGATGGCTGTTTGTGCTGCACTCTGTGCACTGAAG
178	A	T	---	---	TTTCATGCAGAAGGTCCATGATTACAGAATCTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGTCTCATGAAAATTGGACAGCATGTTCCAGCAGAGGAAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTGT/JTTTACTAAACACAAAATGT TTAACITGGGGTCCACAAACAAGGATATGTTGGCAATGGTATTCTGTGATG
76	G	A	---	---	CTATGTTTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCTCTA GAACCTCAG/JATCGAAAGGAAGTTTCATCTAGTCCATAGACCTATCTCACTGACCCAAAAGGTA AAAAAATAAATAAAGTAAGAACCTTACATCAGATTGTGCACTTCTTATTTTGGCCACCTGTTTGT TAGGAA

WI-5791a	44	C G ---			CTATGATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/GIACAAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTGCCCACCCCTGTTGT TAGGAA
WI-5406c	120	C T ---			CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/TTTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAGGAAAGGAAAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAAT GTGGGCTCAT	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/TTTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAGGAAAGGAAAGAGAGGCAA GG
WI-5406a	42	A G ---		---	CACCTGCTGTTGTCCATGGGTGCCACAGACTCTCCAGAAGAGGJGJGCCACTTCCACAGATGCAACAG GCCTTTTGAAGGAGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCTTAGAATTTCTTGACTCTGTGAAGAGGAAGGAAGGAAAGGAAAGAGAGGCAA GG
WI-5798	48	G C TG	TTTATTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAAGTATTTT TCAAT	CCATTCTCTCTCCCTCTCCCTTTATCTCCCTGTTTCTTTTG/CJATTGAAAAATACTGGTT TTCTAACAGTGTCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTAICA
WI-5415	54	T A TTT	TCATCTTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTTAAGCACGATTTGTCTTCATGAATTCATCTTTCAGTTT[A/TTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG[C/CTTAAACCATATTTTGTGTTTA GAAACTCCTGTGGCCAAACCACCTCTTGATGTGAGTGAC
WI-5481b	131	A G CTG CAGT G	TGTCATTTATG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGTAGTATATGCTGAAATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5481a	29	G A AATT	CCAATTCAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTGAAATTTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTCTGTTTTCAAGAGGTAGTATATGCTGAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5492	38	T C ---		---	TCATGAGTCTTCTTCAAGATGCTTGTAAAGTCCCA[T/C]CAAGAAAGGATGCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA

I-5826	134	T C	---			TATTTTTTTTCTCAATTCCTGGAGCACACCATGCCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTTCTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCTTTACTCTTTACAC
I-5546	40	C T A		CCCAATACITTT TTCAGGTGAA		CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[C/T]ACCCCATGTTTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATCTGATGTGGGAAATAT TAGAAAAATTAAGCGAGAGAGGCA
I-5552	97	C T		GGCACCAGCCT TTTTAGAGT	OCAGG	TGTTTGTCTGCACCTCCCAACAGTGGTCAATGAGCCTCAAGGGTTTGTATTGAGCGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGT[C/T]CCTGGGCAATTTGTGCACCTAGTGTGAGA
I-5836b	161	C T	---		---	TAAAGTTGATTTAAACACTCTGTGCCCTCAATTTTCTCACCTATAAAATAAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATCTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C/T]CCATTTTGAAAAATTAAGCTTTTGAATTGTTTTTCCA ATG
I-5573	58	C T		GTTCAATAGG AGGTGGGA	TC	TCGGGTATTAGGATGCGTTCAACCTCGATGATGATGGCGTTTCATAAGGAGGTGGGA[C/T]GACAC ATTACTCTCCAACGTTCATCAGAACACTTCAACAGCG
I-5850b	134	G A	---		---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGCACGCTCTATCTTCTATATGGGCAATATCCAATGTCCCATTC[G/A] TTTTTGCCATTTCTGTATATCAACAGAGAGAGGCTGG
I-5850a	92	C T	---		---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCTCACTCTTCTCTGCTGCCATGGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C/T]GGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGGCTGG
I-5612b	125	A T		CTATTAAATGA GCATCGTGTCA	ACTG	TGCCCTGATTGACACATAGTTATCTGACAGTAAATCAATCTAACATCACAATAATCTTATTTCTGCCTG TCACACTAATTTGCAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCTATTC[A/T]CAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
I-5612a	44	T A	---		---	TGCCCTGATTGACACATAGTTATCTGACAGTAAATCAATCTTAAACA[T/A]CACAATAATCTTATTTCTGC CTGTACACTAATTTGCAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCTATTCACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
I-5636	26	A C		GCCAAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGA	TGAGAGCCCAATTTTATCCGCAATAAA[A/C]TTCCCAAGTCTCTGATGGAGGCAATTCAGAAATCGGG GCAGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

VI-5865c	103	C G ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAAATTAA[C/G]AAATATTATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACTAAATAAATTCACAG
VI-5865b	99	T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAAATTAAACAAATATTATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTTCA GAGAAGACAGACAACTAAATAAATTCACAG
VI-5865	165	T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTGCTCTATCAAAAAATTAAACAAATATTATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGTAA[C/G]CCAGTCTCCATCTTCAAAAGGTCACAGTCCCTC AGAGAAGACAGACAACTAAATAAATTCACAG
VI-5874	76	T G	CATAGCATGG ATAATATTAT ACAGAAAAA	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAAATTTTGTGTAATTTTCATAGCATGGATAATATTACAGAA AAAAAATTT[G/T]ACATATCAAAATGACTGAACTTACTAGTAGCAATTTGTTTGCAATTTGCT CATGGAGCCGACGTTCCAGCTCTCAGTTTTTCCATC[A/T]TTTTTTCATAATTTACTCTTTTTCTGTC ACAATGTTCTGCTTCGTAATTTCAACTCICATTCGTCGATGGATGGTAGTCATAAAATATGGTGATTC AGAAAAATAAGTAAATG
VI-5752	36	A T	TTTTTCCATC	GACAGAAAAG AGAGTAAATT ATGAAAAA	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAAAT[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA CATTGTTGAAAACGAAGCCAGTTTTTCCGATTACACAGTTAGTTGTCGT
VI-5760b	61	C G ---	---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCCGATAAAATACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAAACGAAGCCGAGTTTTCGATTACACACAGTT GTCGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAACGAAGCCAGTTTTTCCGATTACACAGTTAGTTGTCGT
VI-5760	187	G A ---	---	---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGTGTAGACTACTCATTTCTCAGTCTTCCCTTGCTG
VI-5944	52	A G	TTCTCACCATG GGAATCTTG	GGTGCGATCT AACTTGCA	GAGTTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCTCCCACTTCACATTCACAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGATCATTTTCAAGAGTGTGAG TAATGCTTGGTA[C/T]TTGCTCTGTGCCGTATCTGCTCCCAATCACCATTCCACTTTTATTCCTATTAT GCTGAATGAAACGGTTATATTACAG
NI-5967b	148	C T ---	---	---	

VI-5967	165	CT	---				GAGTTAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCTCAACTTCCACATTCAGCAGATATTCTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGTAATTTGTGATCATTTCAAGAGTGTGAGTAATGCTTGGTACTTGTCTGTGCGGTATCTTGTCTCCAATCACCCATTCACACTTTATTTCCCTATTATGCTGAATGAACGGTTATATTACAG
VI-6093	53	GC	---				GGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA[G/C]GTCTGTAATGATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCCAAGTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCCAAACCCAGCGACACTGCTGACATTTGACTTTTACGCAAAACCTTGATTGACGGTGACACACCATGCTTCGAGAAGGAATGAGG
VI-6141	80	TC	AGGTACTT	AGCATCTACA	CTTCTTAATT	TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAAAATTGAAAATTGAATAATTAAAGCAGCTTCTTAATTAAGCATCTACAAGGTACTTA[T/C]CACTGTTCTGGGTTTCAATCCTCTCACCTTTTAGACTTCAGGAAATTCAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGTCTTTTCTC
VI-6450	45	TG	TGTCACA	ATTCTATATCT	CCAATGACTT	TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTCCAATGACTTATTCTATATCTTGTACAT[T/G]AGAAGTACCACACATTTCAACAAGAGCCAGGCTATGCCAGGGTGGGATTATTTTACGGTCAATGTAATATGCATGTAAGACTATTTTACTGGCCTCTTTTATGCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAGCAGTTGTCATGTCCCTCTGGTACTAGAAATAGTCTTTATAGAATATGTGGTTAGAAATAAGCCACA AATTATCTATAAAACAACA[C/T]AAGGAACGAGGCTCAAAAGTGGAACAAAAACGGCCTTAGTTTCTAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
VI-6461	88	CT	---				GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGACTTTCTGGGCTATGAAATAGTCTT[C]ATTCAGTGAAGTATGATCAATAAAGACATGCAAAAACCTTTTACAGTCTTTGTCTGG[G/A]AATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTAGCCTGACAGGATTGTCCTTT
VI-7466c	141	GA	TTTGCTGG	TTTTCACAGTC	TTTTCACAGTC	AGTCGCATGCC AATTATAATT	GAAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTCTTTGGTCACACAGGACTTTCTGGGCTATGAAATAGTCTT[C]ATTCAGTGAAGTATGATCAATAAAGACATGCAAAAACCTTTTACAGTCTTTGTCTCTGGGAATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTAGCCTGACAGGATTGTCCTTT
NI-7466b	80	TC	GTC	GACTTCTGGG	CTATGAAATA	ACTGAA	TGCTTTTAAAAATAACAATGACCACCACCTGACACCATAGTCTGCTCCATTTGCCACGCTTCTCTCAGTAGAATAAGACAGGACTTTGCTGGTGTCTATCT[C]ATTCCTCTCAGAAAGACACTTTGGCCCCCTCATAGGCATTCATAGATATTGTTGAATGAATGTGCTTTTGCATATTGATTCCTACATTTGATACATATCTCAGGAGGGACATTTGGCCTAT
NI-9814	104	CA	---				CCTCTAACAAGAAAAACCTTGACTTCCTCAACTCAAAATACCCTTCTCTAATAATTT[A/G]AGTAACCAAAATATTCCTTCAAAATAAATTAATCTTTTAAATTAGAAAGAAGCAACAGTGTAGAGGTAGTACATTCA
NI-9720b	55	AG	---				CCACC

II-9720a	47	A G ---			CCTCTAACAAAGAAACCTTGACTTCCTCAACTCAAAATACCCCTTCTCTAGATAAATTTAAGTAACCA AAATATTCCTTCAAAATAAATTAATCTTTTAATAGAAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
II-9825	123	A T ---			CAGGCTCTAAGGCAGGATGGCTTATGAGATACTTTGCAITGTCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTCTATGAGGATTAG TAAGATCTCTTTCTAAGACAGGAGAGATTATTTACAGAAGAAGTCAACAGGGTTAGTTTGCAIT TAAGAAATGCCAGTCTTTGTCTGCATCATCTTGAACATTAATCCACATG
II-9748	74	C G ---			CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTTCTAAATTTTATATGTTTACCCTTT GTCATTGCTCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCTGGAATCTTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCA
VI-9943	91	T C ---			TGAGGCTATGATTGCAGATTTGTAGTACTAATACTTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTCTCTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAAATGCAATTCACACCTTCTCTTTTGTCAITTAGGGA
VI-9891	39	T C ---			AGGGCCCTCACAGATCCGTGAGTCAACACTGCCTCTCTCTGAGTGAGCCTGTGAACCCACCCCAAGAC GGCTGGTCATCAGTGTATCTCTCTCTTCCGGACAATATCTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCAATAATCTTGTGTTAAATAATCTTATAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCTTCTACACAAAGGGATTGCAAA
VI-9897b	84	CT ---			CTCAGAAATTTACAGATCTTCCCAAAATGTCATGATTTCTGTTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGTATCTAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
VI-9897a	83	A T ---			CTCAGAAATTTACAGATCTTCCCAAAATGTCATGATTTCTGTTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGTATCTAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
VI-9935b	115	CA ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGTCACACCTCACAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACA/C/AJAGCCAAGAAAAAGCC TGATATTAAAGAGGCACCTTGCAATA
VI-9935a	42	CT ---			AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGTCAC/C/JACCTCACAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTCAGACACAGCCCAAGAAAAAGCC TGATATTAAAGAGGCACCTTGCAATA
NI-9983	146	CT ---			CCTGTTAGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCATTTCTTTGCTTGA TTCCCAAAACCCCAAGGTTCTACCCCAATCTGATCAAAATGCTGACTAGGTGCTGAGGTTGAGGTTAA AGCATTATGA/C/JAGACACAAAGACAAAGAGTAAAGTTGCTGCTCCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

NI-10019	139	A	T	ATCT	TGATGTAATGC TATGTAGCAA	TGATTACTGT GCTTAGGGGA	ATATCAGTGGTTGAGTATACAGCAATCTATTTTGTTTATTATGTGTGCTATAAATCAATGTTCTTA ACATTCAAATAAGATCTTTTGGCTTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAT CTA/ATTTCCCTTAAGCACAGTAATCAAGGCCCTTCTACCCCA
NI-10020b	122	T	A	TTT	GGGAGAAAAG AAATCATGAC	GACTGTTAAAT TATTTAATCAT TAGTCTGG	TTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAAATAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTT[7]/A/AAAAATACC AGACTAATGATTAAATAAATAAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAAGTAGCCCT CCTTAGA
NI-10020a	39	T	C	ATAAATT	TGTCATCTTGA CTCGTATTAA	AAATTCCTTTTC AGAGCCAGTTA AC	TTACTTCATTGTCATCTTGACTCGTATTAAATAAATTAT[7]/C/GTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAAATAGCAGTGTATTTATGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAAATAAATAAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAAGTAGCCCT CCTTAGA
WI-10064b	170	C	T	TTTACATG	CCTTTAGATAT ATTGTGATTGT	ACCTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACAGATATTGTGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG[C]/G/GAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C	A	CAGGGAAGG	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG[C]/AJATTATAATA AATATAATTGCAGAGCATCTCTCTCTATGCACAGATATTGTGGTGACACTCTGTTTATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T	C	CAAACCTT	TCTCTGTCCC CAAACCTT	ATTCTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCTGTCTCCCAAACCTTAT[7]/C/JTTAAATCCATTCAATACAACAAGAAATTTATAGAA TATGCACCATGTCACAAAGACACCCCTTATATTAGT
WI-1319	40	A	T	ATTCTTT	TGGCACTTAG AACATAGTTT	GCCACACACC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATCTTT[7]/JACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGTCTCTGTTTATAATTGGTATCTTTTGGCACAAGAGTCTGTCTGAC AGCTTTATGATCTCTATTTTAAACATTAAACACTGGTCAGATGTGTTTAAACTGTGAACTGCAGC
WI-10316	104	T	C	CTCTT	CTGTTGATTT CTACCTCTATT	GCCTTGGAAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAAGCATCTATATTACCAGTCACCCCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTCTTAT[7]/C/JTAAACTTTTGGATACATTTCCAAAGCAT CATGGTCACTTCCAGTTATGAAAGGATGTTTAAAGCCAGCC
WI-2572	61	C	T	---	---	---	AGTGAGTTGTGCACAAATTTGGAGACATTCTGTGACCCCAACTTAAACACACTTCTCCACAC[C]/JAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

VI-10368	31 C T	TGAAGCAACC AGGCTTGTT	CAAGATATTAT ATTTATTCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAGGCTTGTT[C/T]CTACCCCTCTTAGAGAATAAATAATATCTT GAGATAGGGAGGAGCGCTGAGGACAGTCTGGGTTTGTCTACCCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCGTGATGGATTGCCCTTTCAGGG T
VI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CCTCCGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGACGTCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
NI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCGTGACTAGCGGGTGCTCAATAAATAATATTCTTTTTCATATT TTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATAGCAA[A/C]AGCTACTGGAAGCGGCAAGAAATTTAACCCCT
NI-10567b	82 A C	---	---	AGCGATGAAATTTATATGTTATGCCGTGACTAGCGGGTGCTCAATAAATAATATTCTTTTTCATATT TTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
NI-10567a	60 T C	GGTGCTCAAT AAATATTAT CTTT	AAATTCIGTT GGTGAAATTC TAG	AGCGATGAAATTTATATGTTATGCCGTGACTAGCGGGTGCTCAATAAATAATATTCTTTT[C/T]CAT ATTTTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
NI-11153b	84 C G	CAAACTTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGCTCT C	CGTTGGGAATTTCTATCTCACCTAAATATATGCGTGATTAAATATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTA[C/G]GAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTGACGAAGATGTACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTATT
NI-11153a	33 C A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTCTATCTCACCTAAATATATG[A/G]TGATTAAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGAGTTTTTCTTTTCTTTAATA AAACATGCATATTTAAGTTGTGACGAAGATGTACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTATT
NI-12616	125 T C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTAAACTCCAGTATCATTTCCCTCAACCCAGCTTAAATCACAATCACATTTTCTTTCTGTA GAGCTCAAACTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAAGAAATGATCCTAT[C/J]ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAAACAG
NI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAAGGAAACACACAAAAAGTTTCAACCAAGTGAATATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAACCTCAAAATGAAAGAGACAAATATAGTTCAAAGATTCAGGTTCAATATTTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTTCTTTTCTTTTGT[G/C]CTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGTACTATTACCCCATGGGGTCAT AGAGAGGATTAAACAGGGGTGATGCCCTGCAATGGGAATATTTGAAAACC
WI-10656	59 T G	---	---	

Jl-1169b	154	T G T T T T T	TTAACCAAGA G T T T T C A T T C	CTAACTTAAAA ATCCTCATTC A AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCCTAAAGTAGTGCTTTTAAACCAAGAGTTTTCATCTTTT TTTAAAAAAGAGCAGACACAT/GJTTTATCATGTGTCTCGATAATTTTATATATTTTGAATGAGGATT TTTAAGTTAGCAT
	95	A G T T G A A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCCT/GJAAAGTAGTGCTTTTAAACCAAGAGTTTTCATCTT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTCTGATAATTTTATATTTTGAATGAGGAT TTTAAGTTAGCAT
Jl-1169a	95	A G T T G A A A A A			CAAGTCTGGACCTTGGATAGGTG/GJACCGGCTGAAGGTTGGACAGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTATAATAGATCTTGTCCCTTTGGGTTTACCACCTAGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTGTCTAAATAATCCAAAATAGCCATGGGTTGGACAAAATAC AAGGTTAGTGCTCTCTAACTTTAATGGGCATA
Jl-10685	25	A G ---		---	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTTATGTAAATATTATGAAA AAAGTCAAGAGAACAGATGATATAGTTCTGTAGAACTACTTGAATCTGATGCCCTGTCCAAGG C/TJTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG
Jl-10686	133	C T A A G G	TGCCCCGTGTC T A A G G	CAATCTCTAAA TTCAATGTGTAG ACACA	GGTAGGATGATTCTAGAAATGCCACTTACAGCCACTGAAATATATGCCCTCCCAATGATCTTTCTG CTCAAAGAGT/AJTTTTTAAAGTTATCTACTTATTTATCTGCTTTTCAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAAGTAAGAAAAAGAAAGCCCAATT TGCGC
VI-11175	77	T A A		AA	TAGAGAGGCTTTTCAGTTTCAGGGTTGGAGGGTGGTGAGGTGAGATTCACCTTCTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTTCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT T
VI-10694	144	A G T A T A G A T T T C	TGCAAAATGCTT T A T A G A T T T C	GGCATTTTGT A AAGGAGGAAA	GTGAATTCATCCAGAAAAACAGCT/C/GAATGACAACAAGAGAGAAAAAGAGAAATAAAGGTTTTGT ATACGACAAGTGCTCAAGCAATTTCTCTGTCCAGTGCATGGAGCAGTG
VI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTGTCA TTC	CAGGCCAACTCTGTCAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTCTCTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCCATAACTAA
VI-10719	115	T C G C C A T T C T A G	TGACTCTCAAG G C C A T T C T A G	GCACTGCCAGC AGCC	
VI-10721	40	A G C T T G C C A		GAAACTCCAC ATAAATAAT CTCA	CAACCAATTCAGATTTAAATTTTGGCTCTGCTACTTGCCA/GJATGAGATTTATTTATGTGGAGTT TCTGAAGATCCCATGGTAAATAGTATCCCTCTCCCTGCTTAGTTTGAAGAAGTTGAA

VI-1204b	88 T C ---			GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTACACCTTTTCATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAAATTATTGAGAAG GCAACATC
VI-1204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAATATTGGCTGACTTTGAGGAGGAGAACACAGGGAGTTGAGGTAAAGGGTG AAAAGAAAACCTTTTCATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAAATTATTGAGAAG GCAACATC
VI-10732	80 C A ATTGGTCACT	GCTGTGCTTC GCTGTGCTTC	AAGAACAAATG CATAACAGAA CTTTAA	ACATGTATTTCCTTAGTGGTCAGCCTTCCCTACCCCAAGAAATATCCCTGGTTATTGCTGTGCTTC ATTGGTTCACCTTCATTAAGTTCTGTTATGCAATTGTTCTTGAGTCCACATAGGTGTTAATCAATTCCA CACCACCTGTTTAACTGTC
VI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGTCTATAAAGAAATTACCACCTCTGTACATTTTGTAAAGATAGCACAG AGAGAAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACTCATTCCAA CCATTAGGATTGTCACCTCATATATAGACAGAAATTCAGTGTGGTGTGATTGAAATTCACACATGGA ATAAGTCTA
VI-11215	68 C T ---			GAAAAAAGTTTTAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTCAGATTTATTTTAGT TCATTTTCTATAATATTTTCTGTAGTGTGATTTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATTCAGCCCATTCACCATGT TTT
VI-1219b	89 G A AGAGAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAATTTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/A]AGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
II-1219a	18 G A ---			ATGAAAAATGCATTAGAA[G/A]AATTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAACATCTC
II-1222b	136 G A GGCTGG	CATACCACTGC AGCTGG	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGGAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCGTTGAACCTATTGTTAAACATTTACCAGCATACCCTGCGGCTG G[G/A]TCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTTCACAGGCTACTGG AAAGCC

1222a	25	C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTCG	AGCCACAGTGAATCATTTACACTA/C/TJCGAAATCAGCAAAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTTTGTTTTCCATAGACCCACCGTTGAACATATTGTTAAACATTTACCAGCATACCAGCTGCGG CTGGTCAACAACCTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTCGTTTTCACAGGCTACTGGA AAGCC
1-10775	39	C T C	TTATGCGCATA TTAATTCAATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATGCGCATATTAAATTCATTACACTC/C/JACATCATATTTTCTTAGCAATACA TCTAGACACCTGGCACCTCAGTAAGGGATATTCTGGCAGGATAATCATTTGTTATCATTTAGACATTGCA GGAACCAACCATATGGATGGATAAAATGTGTTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATAAATATCTCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAATACAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAATTTGCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/C/JGACATAGTTGCTAAGGATATTCACACAAATTA TTCATGA
1-11226	165	A C ---	---	---	CAGTGGCTGGCTACTGACAAAACGTAACTCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/GJG TCCATCTGTGATGTCACAGCAGGCCAGGAAGGTTGATCTGGAG TGGGACACACTGCTCTAGACC/C/JTCCCAGGGTCCCTCAAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGAGGCATCAGGGCCCTAGTCCCTCTGGGACAGTGAAGGGCCACCACC ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGAGAAAGCATCTTCATGGCAGGAATTC/TJCATTT CTGTGTTTCTTAGGGTTTGTGGCTGGCCATCAGTTCAACTCAGCCCTGTCCCTGTATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAAAGAGAAATGATGA GGACCAAAACAGAATTACTTGGCA/T/CJAGGGTTTCTTAAACCTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATATTTGGATACATTAGGCTCATTTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
1-10828	23	T C ---	---	---	TATGCCITCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAGAAATACATCTCTGAATG GGCACATTAATCTGCAGGCTCTCC/C/JTCTTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAAAGGCTGCTCCGTGAAATAC TAGTTCGG
1-10832	91	G C AGGCTCTCC	CATTAACTCTGC AGGCTCTCC	A	GATTTGAGTATTATCAAAATGCCCCAAGACCATTAAACAGATTTAATAGTTAAAGCCAAAACATA AAGAATTAACTGTTCAAAAGTGTGTTAAT/C/JCTTAATACCAATTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAAGCATATGCAACTAAATTTCTAAAGTCCAGT
1-10834	96	C T GTGTTAAT	AGAAATTAAC GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GGATGATGTTCTGTGGTCCCTTTA/T/CJAAAGCCCTTGTGCATCCCCAAATGTGTAATTTATTCT TGGTATTTCTCGCTTACCCTAGTACCTGTCAAGTGTCCACCCT
1-2287	24	T C ---	---	---	

VI-2296	81 A	G	TGTTACTTTGA TTCTTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTTAGAAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTTGCAGAAAGTTACATTTGTTTGTG
VI-2300	77 G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTCTCCCTGGAAATTTCTTTATTTGAGCGGGCAGGTGGTAGGCACAGAAAGC CAGTCATAC[G/TT]GCTTTAAATTTGACCCCAACCATTAAGAAATAGCATTTCA
VI-2371	55 G	T	GTCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGCTGGTCTTGTCTTCCAGCTTCT[G/TT]GTGGTGGCT GTCAATCTTTGACATTCCTGTCTTGACGCTGTATAATCCAAATCCTTGCCCTCCAGCTTTACATGATGT TCTCTCCGTGTCTGTG
VI-2395	122 A	C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTTAAAGATAACATAGAATATCATATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTAATCTATCCAA[A/C]CTGAATTC AGAATAAATAGAAAGGTGAATCATCTTATATCATTTAAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCA
VI-2437c	192 G	A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCACAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
VI-2437b	179 G	A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCACAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
VI-2437a	128 G	A	---	---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCACAAAAATTCCTCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
VI-2440	71 G	A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTGTC TATTGGTCTCA C	CAGTAGGAAACGGGTCTTCTTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
VI-1356	123 T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACCT GTACCAAAACAT G	CTGTAAACCTACACACATCCTCCTGTAACTCTAGGTTACTTTGTAATACAAAAACACAAATGTAATGCT ACATAAAATAATTTGTCATATACTATATTTAGGAAATAATGACAAAGAAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCCAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGTTTAAATCCACAG AAACCACGAATG
VI-2886	46 C	A	CAGAGTCTGG GGGAGAAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGAGAAAG[A/C]AAGCAGATAAAGCATG GCAAAGACCACCGTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGAGAAAGAACAGAGGAGCGTT

VI-2906b	77 T A ---				CCTGAACACCTGGAGCACTTCCCTCCCTGGACACCTTCATCTTGCTGGAACCTTGCCTGGAATGCTC TTTCCCTC[T/A]GAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTAGAGTTGGTTTGGTACCAACAAA
VI-2906a	50 A C TCTTGCTGG	GACACCTTCAT		AGACATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTGGACACCTTCATCTTGCTGG[T/A]C/TCTTGCCTGGAAT GCTCTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTAGAGTTGGTTTGGTACCAACAAA
VI-1736	175 C T ---				TACTCCTCATCTCCTCATGTCCCTAGACGTACTCAGATTTCCATGCCCTGAAACATTTATTTCCCTAAAT TAGATTTCCACCCCCAGCACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGTGTTTCCCATCTGCTTCCCA[T/C]TAGAGATCTAGGGTGTCTTTGGAAACC ACCTTGG
VI-1851	136 G A GTGTTAAGTA	GCATTGAATT AACTATAGAT		CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAATCTGGGAGG ACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAAATTATTAACATGGTA CA[G/A]ACAACCTCAGTTTAACATTTGCTAGTGATCCATGGATACCATGTACCTTCTTACATCATG TGA
VI-3000	62 G A AGAGACCCC	CCCAAAACAC		GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTGAGCACCCAAAACACAGAGACCCC[G/A]T GAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
VI-1754	177 G A TAGTC	TTTTCTCCCTT CTTAAAGAGA		AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACT TAAGGGTTTAGCAAAATTCACCTGACAAAAGAGTTAGGTTTCAACATTTGACCCCTCATAAAGTGATTTT TTCTCTTCTGTTTGTCTTCTCCCTTCTTAAAGAGATAGTCT[G/A]CCAGAGGCAATTCGACTTTCTGT AGCCACAAGATT
VI-3167	37 T A TAGATTC	AAATTCAACC ACAGATCTAT		TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAAATTCACCAACAGATCTATTAGATTC[T/A]CACCCATCTCAAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
VI-3208	140 G A AGATAAAGA	GTGGAGTGGGC		TCACTCAAACT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCAACTTGGCGCAGAGAGGGAAG AAGTTGAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTGTAGGGCAGGTGGTGGAGTGGGCAG ATAAAGA[G/A]CCAAGCCCTAGTTTGAGTGACACTGTGGGGATTCAAAG
VI-1775	47 C T TTTTCTCTG	CCTGCATGGTC		AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG[C/T]TTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
VI-3402	55 G A ACAT	AGCATATTCA TTGATTTCCCT		GAGGACTTAAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTTCATTGATTTCCCTTACAT[G/A]CAAATGCTC CTTTTAAGTCCCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCAATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCAAGTTGTAGCATTGAGAAGTC[C/T]CTCTTAGAGGTAGTTGCTCGTCTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACCTTCTCCAAACAAGTGTAACCAACAGCATTTGTTAAG GAAATGTGAATGCTTGCTACCTCTGACGCGACAACATAATTAATCCCATTTGCCTAAAAAGACCAGG
WI-3453	70 C T	TTCTAGGCCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAACAACAGAAATTTAACAAATTTGAAATCAGCTACTCTTCTTAGGCCCATCAGAG AAT[C/T]GAAGTCAATGGGGAAAAATGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAGAGAC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT[G/A]TGGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAAACTTAAATCATCAAGTGTCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC/[A/G]GTAATTTAATGAGGTGGTGTGGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCACC
WI-3502	79 C T	CCTGGGTTTCT GGATGICT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAATAAAACCATAAGAAATGGTGGAAAAATAAAACGGGAGAGACCTGGG TTTCTGGATGTC[T/C]TTTGAGGACAGGGTCACCCAC
WI-3600b	146 G C	GGTTTCTAAC TGGATATAAA CATCT	CCAGTGCAGOC TTCCAT	TCACGGCAAGTTCTGCAGAGTGTCTTGACTCCTGCCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG[T/G]GAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT[G/C]ATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCCTGCCTGTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG[T/G]GAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3678	125 G T	---	---	TAAATCATGCTTATTTTCAAGGTAATCCACTCACAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCATGCTCTTCTGAACTTCTACTTACTGTGCTGTTATGATGCACCT[G/T]CCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAATTTACCTGTGTGTTTCAGGCAGAAATAG ACTCTCTCTGTGTAATCACTGAATGAGTTCCTGTTTCAAGGCTTTATGCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACACAAAAATGACATAAAA T[A/C]AAAAACTACTATAGTTTATGAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACCTAAACAGG ATTCTCAATTCAATCCAGAACTACTCCTCTGTCAATTTAACTTTGACTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAATGA CAAAAC	GGCTCACCAT CATTTT	TCATAAATGTGAACCAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT[C/C]ACACCGTTCAATGAAAAAACAAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGGCAATTAAC

WI-1819	51	CT	---			GAAAAAGCAGGAAGCCAGGCAGGACAAACTTTTGAAAAAGTCTTTCAGCAC[C/T]TTCGTGGATCCG AATTTAGTGTGATTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCGAATTAATGAATGTGAAAAAAGGGTGGTAACTGTT AAGCTGCTGCAATGTTTAGACACGAGGGTGGGGAGGTGGAATACC
WI-3746	116	GA	---			GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAAGTAA ACTGCCCTGGCCAGGAAGATGGTTGCTTTCATCATCTCTGCTCTG[C/GA]GCCCCAGGATAAAGCA GGCA
WI-3867	49	TC	CAA	TAAGATAACC ATACTAGGTAC ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTAGTCTTCCCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTGAACAAGACACAGT CATTAAAGTGAGGAAGCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	AC	G	TGACCAATGTC TTTGAAGCA	TCGTGGTGTGTC CTCTOC	CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCCGACGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGAGCCACAAAGGTGAGGAAGCAAGGGTGTCTGGCCACT
WI-3901	114	AG	---			GGACCAATTGTCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTCCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGTAACCTCGGCTTCTCACCTGACAAAGTGGA/GTATCATGTGTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	CT	GC	TGATCTTCTC AAGACTCACA	TCTAGAAGCAA TGAAGGATGG	CTGAGGAGATTGATGCTACTTTACCIGAGGAACCTTTTATTACCTCCCTGAGTTGTTGCCTTGCAA GACATTGCTGATCTTCTCAAGACTCACAGC[C/T]ACCATCTTCTTCTTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAGGTACAAAGTGACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	GA	A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG	CCACTCCAGGCCAAGAGCGTCCTATGAATCAT[G/A]CATTTGTTCTCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	AT	GT	TTGAGGTCTTA GTTCATTGCATG	TGAGTTCCCTAT TAAGTGACAAT ATTGTT	TAATTCACATTGCTCTTGTGTCATTTATTGCTTCTCTTATGTAAACACAATCACCACACATTGAGG TCTTAGTCATTGCATG[A/T]TGTAACAATAATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTT ACATTTATTGCTAACAGCAG
WI-4160	117	AG	CAACAGAA	CCATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC	TCCCTCTCTGTAATAGGAAGTCGATTAGATGCCCTTTGAGGTTAGGTGGCTTCTAAGATGGTAATT ATCTGTCCAAGTTTGTCTTCTTAAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCTCATGATACT
WI-4168	32	AG	AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

II-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGATATACCTTTCCAAATGACTAGTAGTAATAAGCACGTAATTAATTTACCTATTATATTT AT/CJ/CATCATGATTTGCTGCTTCTTTCCAAATTTACTACAAATTTGATTGTGCACATGAGGCACATG ATCCCATTAACCCAAATAG
II-4199	51 A C	CTCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAAACCACCTCCCAAGTTAGTCAATATAAAAAA[AVC]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAACAA
VI-5163	24 C T	CTGTCACTGGT CTGCCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCTGT[C/J]GGTCTGTTCCTGTGTTCCTTTCAATGTTCAACTGCTTGTAT CTGTGCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGGCTTTGTAGACCAGAGTTTCTT GGAATTGCAACATTTGGGCAT
VI-4250b	117 A G	---	---	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGGGGTGGGAAGGATCCTGTAAAAGG[A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
NI-4250a	94 G T	TCAATATGAG TCITGTGAAAC AGG	CTTTACAGGA TCCITCCCAC	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTCTCCACCAGTGCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGG[G/J]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
NI-4255	68 G C	TGCTCCCCCAT CACCT	AGTTGTGTAAG G	TAAATGCTCTGGGAGATAATAGAAAGTCCCATCCCTCTGATACCTTGGTGTCTCCCCCATCACCT [G/C]CCTTACACAACCTTGAAGTAGGCCCATCCAAACACTGGTCAGAAAGTAATACTGTGCGAC
NI-4256	57 C T	---	---	ACAGCCTCTTCAAATGGCACAATCAAAAGCACCCAGTAAAGCAGAGGCAAAATCTGG[C/T]CTCAC CATGGAAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGAATGATTGGCCTT
WI-4325b	71 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGTACATGGGCAGGACCGGAAATGG GAT[C/J]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCGCCAC CCAGGCACACTGCCATACT
WI-4325a	58 C T	---	---	AGTTCACTGCCTAGATGAGTAGACCATGTTGCTTTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCGCCAC CCAGGCACACTGCCATACT
WI-4347	158 A G	---	---	TGGGCAGAAGTCGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCTGTCACTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCCTCCTGAGTTTATCATCTCCACCTCCAGCCCCAG GGCCCTGTATCTGTTCAAGGCC[C/J]GJAATCGTCACGGCTCACAACTGTGGAGGTAGGAATGACGA G
WI-1936	117 T C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTTCTGGGGCAAGTCTGGTGTGTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACCGGGTACTTGTATCACC[T/C]CTCCCCGCAACCCCA AGCAGCACAGCTTGCAGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGA

-5204	54 C T ---			TAGATTTGATTGATGACAAATAGGGAAGCCTTTGTTAAATTGGGTTTTGAAGAA[C/T]GAAGAAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAAATCCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
-5215	70 A G C T C A A A A A			TTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTTACAAAATATCTCCATAGCAAGTAGACATTTTGGCACATTTTCCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT
-4448	112 T G A T A T A A			CCCTGAAATGTGCTTTGCTTCTCTCCTCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTACTTTTAATTAACCTTGATCAAGAGAGATGGGTATATAAT[G/A]AAGAAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
-4456	49 C T T A T A G T T C C			ACACATTTCAATTTGCTTTAAGTTGAATTTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAAACACCCAGGTGGGCAATTGATTGAATTGT
-4461	49 A G C C T T C C			CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAATATCCTTCC[A/G]TGAAATTTGGTGAAA GGTCAAAAGAAATGAAATCCACCTTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
-4465b	75 G A ---			CTACTGGATTTTACTTTGCTCAAGGCCAGACACACGAAAGTATATAAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTTCTACCTCAGGGAATC
-4465a	41 A G A C A C G A A A G T			CTACTGGATTTTACTTTGCTCAAGGCCAGACAAACACGAAAGT[A/G]TATAAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTTCTACCTCAGGGAATC
-1949b	160 T T C T A A T C			GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAATTTCAAAACCAATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAATAA GGAGTGAATAAATGAATGCCATAATC[T/C]CTGTGTTTTTTTGTCCTCCACCTCTCACACCTTTCCCTGG CACA
-1949a	86 T G A T G C T C T G A G T			GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAATTTCAAAACCAATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/C]CAAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTTGTCCTCCACCTCTCACACCTTTCCCTGG CACA
-4529	64 T T C A A G A T G			TGAGAGAGTTTTTGGAATTATTCATCCTCTGCAACACTCCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTCTCTCTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTAGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGCAATGGCTGCATTGTCCAGTC AAATGAGACAACTTCCCTAT
WI-4582	226 T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATTAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAACTCCAGTAGCAATTCAGGCCAGTTTAACCTTATTCCTGTACACA ATAACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAATGACTCGGTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT[C]CCTCCTTGCTAGAAACCATTTGAT
WI-1965	105 G C	GCCATTGAGG AAGTGTTAA AG	GAATGGATGGG TCACTCTCT	CAAGGTTAGTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCAATTGAGGAAGTGTAAAG[G/C]JAGAGAGATGACCCATCCATTCCCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T	CACTGTTTCT ATTGACCGTAC TTG	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGT[A/G]CJAGCAACCCAGAAAAATTAACACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG[C/T]TCTTTGCTTTTTTCCCTTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38 G C	AGTTGTGCTG CTACGTTGT	TTTTAATTTTC TGGGGTTGCT	TGTTTAAAAACCATACAGTTTGTGCTGCTACGTTGT[A/G]CJAGCAACCCAGAAAAATTAACACGCCTAC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTGCTTTTTTCCCTTCTCTCTTTTTCTG CCCTCTTTTAACTATT
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTTGCTCTGAAAGCAGAAAGCACTGTGA C[T/A]CATTATTAGGCCCATCTCCTGCTGAAGCCTGCCTACAGCAATTTGTAAACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTGACAAGATTCTCTTTTTTAAACA
WI-5252	119 A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAACTTGGGAAAAGGATTGTGATGATCATTG AATCTGTTTAAATACAGAATTAATACTGAATACCTGTGTGAATCATTCCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G	GCAATGCTAG AAAATTATGC CT	TAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAAGGAAAAATGATAACCCAGGACTGTTGTTCAAGCAATGCTAGAAAAATTAATGCCTA[A/G]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTCTTGTCAATTAAGTCCTCTATTCA ATTACCATTTATCGGGGTAATTAACACACTGGAAAGTAATGCCAGGCTAATTTGTTAGATTATGATAAT TACACGCTTTGCTATGCT
WI-5257	77 C A	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAAGTTACCAAGATCGGGGCAAAATTAAGCATATGAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGG[C/A]CTTTCATCTGCCCTGGTGGGTTTTTCACTAAGTGCACAACTGTCTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATTCACCTCCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T	GAGACCATCT TTCCGAATG	TGTAAGGTG TACTTACAAGA AATCATC	TCACGTGTTAGAAATTTCTTCTCCTCAGTGAGACCATTCTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGTATTTTTTAA AAATCCTCCCAATATG

-4650	148	A	G	G	CTCTCT	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGTGATGATTGTTGTGATTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAAGCACAAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTTAACTTCAGTAAACGTT
-4677	82	T	C	AAA		TCCAAAAGTG ATTAGGTGAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACACAGCGTTTATAGGGGAATACTCAT
-4698	135	C	G	---			---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTTGACGGAAGAAAACTTCAA[C/G]TTCGAGAAAGGCTTAGATTATATCGCTGAAGCCCATCTG
-4722	88	G	A	AACACCACAC		TGCACATATGG	AATATGGAATC TGCAATTCAGTT G	CTTCCCATTCTGCCAGTTAGATGACTGCCTCTCCACCGCTAGAAAAAGATGGGAGATTATTTTC TGCACATATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATTGAATACTGGGAAATCAGTGA AAG
-2020	145	C	A	---			---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGATTGTCA TAAAGGTCAGTAAATCACTTTGATGGTTGAGATTTTCAAGAAACGTGAAATATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAACACAGCAGTGTGCTCTAAAAAATATGATAGTTTCTCTCTGTCACCC GCAATGAAAAAGGAGTT
-2028	176	T	C	CCTGCTCATC		TGTTACGTTT CCTGCTCATC	GGTTGGAAACT CAAAATTACCTA GAA	GACTACAGCGCACAGACAGGCGATTGTGTGGCTTGACAGGTGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAAAGTGGCTCTTCAGTTTACTACAGACCTCATCTCTGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGCTCATCT[C/T]TCTAGGTAATTGAGTTTCCAACC TGTTG
-2033	183	T	C	A		GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTGCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTCCAAGTTATACAGGACCAAGTTTGGAAATTT AGCATTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAACCC ACTGATATAACCAAT
-4745	131	T	C	---			---	TTATGGATACATGTTTCTGGTGAAGGACAAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCAAGGCTCCTTCCACCAATCTCCATCTACTCTGAT[C/G] AGGCAGACTTATATGAAAAAAGGGA
-2034	150	T	C	CCAAGGAC		CCACAGTGCA	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGCGGTTTCAAGTGAAGACGATGAACCTCTCATCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAC[T/C]GGACCTGCACCTCTATCTTTACCCCTTCCGACACCAAGATGCTGAGATGCC ACACTCTGAGTG

I-2038	155	C T	TGTCCTTTAAA GTGTGTAAGT ATTAATTAG	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAGTCACATTTCTTCAATCACTCACCATTGTCTGTATTGTCTCTGCAGTGT ATCCAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGAAGTATTA ATTAGATTCTATTTTGATA[C/T]GTGATGTTCTTTCAAGAGGAAAATTTGTGTAAAGAGGATTCCCATTT TGCAATTTCCATTGGC
I-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTTCTG GTTATTTTCT GTTC	TCATTGACTTTTATAGAGTCTCTCAGTCTTTATGTCTTATTTAGGAAAAAAGTCTAGGCTAGGAGAA CACAAATTCAGGTTCTCTCCAGATGCAGAGATACTAGAAAATGC[C/T]GAACAGAAAAAATAACCA GAAGAGTTCAATTATGGTTTTTCCAGAACGATTAC
I-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAATT AAAATTTTGGC ATAA	AGGAGAGTTTTGGCTCTTTCCGGACTCTTGGAAATTCAGTGCATAGAAATCATCTTGCTAAGTTCC[AG JTGAAAAAATAATGCCCCAAATTTTAAATTTTATCCAAACTTTAAGTCGAGATTATAATTGATATTT AAAAAATATATTGAGTCTTTCTTAAAGAGATGGCGTATCACTCTA
I-5300	38	T C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTCATAATC CAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCACCTTCATTC[C/T]TTTTGGATTATGAATAGAAAAGAGT AGGTGTTATTATCTCTTTTACCAAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCCA AGTCAGTGACAGAGCCA
I-4818b	121	G T	TGATAATGGG GCCCTGTT	CCTTCCCTTTA TATGTATGCCA GA	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAACTCTTATATA ATAATTTATTCAGAAGGAAATATACATATGGGGTGATAATGGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
I-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC G C	CATATGTATAT TTTCTTCTTG AATAAATT	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCC[AG/G]CACATGAATAAACAACTCTTAT ATAATAATTTATTCAGAAGGAAATATACATATGGGGTGATAATGGGGCCCTGTGTCTCTGGCATA CATATAAAGGAAGGCTAA
I-5317	139	T C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTTCCATTTTGTGATTCTTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATATTACAATTTCAACTCAACAGGAATTCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTTTGTCATCTATTTCTAGGTTATTTGAGCCCGAGATCTACCCAGG
I-4888	56	G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATTCACCTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAATTCCTTGATAACTGGAGTAGTGCCCTT
I-5328	44	A G	---	---	AACATTTTTTAACCATGCTACATTTACAAACACTGAAAAGACAG[G/A]AAAAAAGAAATATTTTG CCTCAAAAAAGCTCTTAAGAGATTATGTAATAAAAAAGAAAAAATATGAATCAGAAAAAGGAAAAAAT AGAAACACGTGATACTGGAAGGAG
I-4897	93	A G	---	---	GCCTTTTTGAGTTAAGTCTTTTGTAGTGTGCTTTTTTTTCCCCCACTAGGTACTCTCTCGGCCCAAT CCCCAAAAGAAAAATAAGCGCTTGG[G/G]GATAAACACATCTTC
I-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTTAAAATCCT[G/A]CCTGCTATGGTTTGTGTTGAAGCCACATCCACT GAGGTATATTCTGTCTGCAATTTCTATATCACTCAGCTTTCAGATCCACTCCATCACTTGCAG

3R- J04W22	232	C A ---	---	GGATAATCAGTACAATAATGGGACCTTAAACTGCTGTGATGCAGGAGTGGAGGGCTGGCAGTG CCCGAGGCGAGGAGGACAGTGGGACAAAGGATGCTCAGTGGTGAGCCACAGCCCTGGCTCTGGA TGGGCATGGGAATGACCAGGTTCCACATCATGCACAGCAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTGTGCTGCCCCCGCCTA/C/A/CTGGAGATGTCTCTAAAA
3R- 005D24	138	C T ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATTCCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAATAAACCCTTTT CTC/T/TTTACCACTTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
GR- 005D24	123	A G ---	---	CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATTCCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCACACATCTTTATAGAGAAATAAACCCTTTT TTTCTCTTTACCACTTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT TTATGTTAAATTCATAAACTCCTTCACCTTTAATAATTAGGAAACAAT
				TGAGTCTGAGCACGAGTTGCAGCCAGGOCAGTGGGAGGGTCTGGGCCAGTGCACCTTCCGGGOC GCATCC/C/G/TTAGTTTCCACTGCCCTGTCAGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGGA GTTGTTCAAATGTTCTCTTTAA
103735	74	C G ---	---	GGTTTGTCTGGCATAGCCATGCTGTAGCAAGAGAGAGAAAAAT/C/CAACAGCAAAACCAACA CAACCAAAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTATTTTTCATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTCC
139840b	42	T C ---	---	GGTTTGTCTGGCATAGCCATGCTGTAGCAAGAGAGAGAAAAAT/C/CAACAGCAAAACCAACA CAACCAAAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTATTTTTCATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTCC
139840	56	A C ---	---	GTGGCCATCGATCTGGACCGTCCCTGCCACTTGTCTCCCG/G/A/TGAGCACTGCGTACAACATCCA AAAGTTCAACAACACACAGAACTGTGTGCTCATGGT
VI-8997	41	G A OCCC	AGTGCTCA	TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGTCAAGAA AGCACCAGTTTCATGATAGGCAGTTTCAGTGCATATGTTGACTTGTATGACCCAGAGTCAACATTCAG TTTCCACCAAGCCCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG/G/JAGAGAGTAGTTATCTGCAGA AGATGGCAGGGCTTGTCTCCGAAAGCCTAGAGACCCGCTGTTGATTACCT
NI-7008	180	A G ---	---	GGTCCACGAATTTGCTGGGGAATCT/C/TGTTTTTCTTCTTAAGACTTTTGGACATGGTTTGACTCC CGAACATCACCGACGCTCTCTGTTTTTCTGGGIGG
WI-9005	26	C T	GGGAATCT	TCCCAAAAGTC TTAAGAAGAA AAA

593	46	G A	---	TTTGTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG[G/A]AATGAGATCAGTTTTGGA CACTTCCTCTTGAAATATAAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCTCCAA
962	78	A G	---	AGTGCATCTTGGGGAAGGCTCCAGTGTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTT GATCCAGAGA[G]GACAAAGCTCCTCAGTGAGTGGTGATATATCCAAGACAGAACCCAAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTCTATCCTATCATAGATAACATTTCTCCACAGCCTCACTTCATTCAC CTATTCTCGAAATATTCCCTGAGAGAGAACAGAGAGATTAGATAAGA
059	43	C G	AAGGACCCA GCCATC	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAAATATACCTGGGTGAAATATACCAAATTTCTGCATCTCCAGAGGAAATAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
063	53	A C	CACTTCACTGA AAGACACCAT TT	AGCAGCCATCACATGATCTGTTTTTCAACCATTCACTGAAAGACACCAATTTAT[AC]TACCCAAAGGG CAGAAAGTAGAACCTTACTATTCAATAATGTTTGACACAAATTGGAATTGTC
079	293	T G	---	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCCACATACCATCTGTAGAGTTGGAACTCAT CTTTAAAGTTTTATGTCATATATTTAGGGCTGTAGACTTACTTCTCTATTTCTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTATACATTTATACATCACCTTTTGACTTTTCCAAGCCC TTTACAGCTTGGCATTTCTCGCCTAGGCCTGTGAGGTAACCTGGAT
074	38	A G	GGTAAAGTT CTTTTGCTCT AAAAG	TGGATGCCGAGGTAAAGTTCTTTTGCTCTAAAAGAA[G/A]AGGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACTGT
104b	249	C T	---	GGAGTTGCCCTTCTTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCGGTTCTACTTTGGACTGAGAGAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCCAGCAAGAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCCTTGCAACCAGGTGGGGCCACAGCACGAGCATCTTTG[C/T]
104	157	C A	---	GGAGTTGCCCTTCTTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCCTGAGGGCAGCGGTTCTACTTTGGACTGAGAGAGGGAGCC CCAGGCTGGAGCAGCATGAGGC[C/A]CAGCAAGAAGGGCTTGGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCTTGACACAGGTGGGGCCACAGCACGAGCATCTTTGCT
1974	34	C T	CCTGAGCCCTC AAGAACTCA	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
3161	61	C T	CCTAAGCATTG CCTGGC	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCAATTTAGTTGCCTAAGCATTGCCTGGC[C/T]TTC CTGTCTAGTCTCTCTGTAAGCCAAAGAAATGAACATTCCA
3014c	93	T C	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCCAGTCATCTTTCTGTTCCAGAGAGGTGGGGCTGGAT GTCTCCATCTCTGCTCAACTTTAT[C/G]TGCACTGAGCTGCAACTTCT

JI-9231	32 C	CAGTCCCCA GATTGA	CAGTCCCCAC ACTCAGAC	GTGACCCCTGTGAGGTCAGGTCGCCAGATTGA[G/C]GTCGTGAGTGGGCAAGTGTGTCAAAAGGGGG TGCCCCCAGGAGATGAGGCTGAGAGCAGGGAGTTGAGGCCGAAGAAGTCA
JI-7836	120 T C	CAAATAAACA ATGCAACGTT C	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTTACTGAAAGAAACTCTGCTA GAATGATAAATGTGATGGTGTCTATAAATCCAAATAAACAATGCAACGTTCC[C/C]GATTCTTAAT CTTGTTCTGAGAGCCATTGGTTTCAGTTGTAGCAATCCCCATACCAGCT
VI-7286	65 T C A	CAGCTTCAGCT TAACTGACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCGATTCCTTTTGGCCCTGCAGCATGTCATGCTCCAGAAITTCAGCTTCAGCTTAACGTGACAGATTC JGTTAAAGCTTTCTGGTTAGATTGTTTTCACCTGGTGATCATGTCCTTTCCATGTGTACCTGTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
NI-7858	91 T G	CTAAGCATGT ACGTGAATTT TAAAT	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAATTCITGGAAATATCTCAAATGTTAATAACAATAATGAATTTTTCTCATGCACTACTATTACTACT AAGCATGTACGTGAATTTTTAAATTT[G/T]ATAGATGTAACACTTTTAATAAAAAATGGGGTGTGG
NI-7860	50 C G	CGTACCTCCAA ACATAAATTGA TTC	---	GAAGATTAAAGGAGGGGTGCTCTGTGGTCTCTCCCTGCCCTCTCCCA[C/A]GTGGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCTGGACCAGTACTGGCCTTATGGGTGGGGTGTAGGAGG TGAGCGTAAGTGGGGAGGGAATGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTGCAGACCAG ACCTAGGTGCTTCTCTAGGAGGGAACAGGGAGACCTGGGGTCTCTGTGGAT
VI-9064	29 A G	CGTACCTCCAA ACATAAATTGA TTC	GCTTGAGTGA AGTCTCGCAGA	CAAGCGTACCTCCAAACATAATTGATT[C/A]GTTATCTGCGAGACTTACACTCAAGCAATCCTGAGG AATCTGAGGGAGGGCCTGGCTACTGCTCTCTGCACCTCTGCTGCTTG
VI-7307	128 G T	---	---	CACACTTGCTGTTCTTCAGTGTGGAGGTCTCGCAGGTCAGGCTGGGGTAAGCCGGGGTTCACCA GGCCCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGGGGAGAGAGTCCCTCCCTCAG[G/T]AAT GGAGGAGGGGACTCCAGGAATGGGGAATGTGACACCACCATCTGAGCCAGCTTGCAACCTCCAGT TTGCACAGGGATTGTCTGTTGGGGCTGAGGGCCCTGTCCCCACCCCCGCC
VI-9274	25 C T G	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCGTGCCATT G	GAGGAAATGTGACTTCACCTTTGGT[C/T]CAATGGACAGAAAAATTCACCTGTGTACATAGGAGAA GTTTGGAAATGCACCTAATAGCTGGTTTTACACCTTGATTTCGAGGTGAAA
JI-7313e	266 T C	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTCTTAAAT TGTTTTGCAGTCTTTTATGTTTTATTATCATAGGTATAGGTGGACCTAAATTCCTATCATATCTTATT AATTCAGCCAGTGTATCCACAGTTTTTGTGTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTAACTGAATAGAATTGTATAGCGATGA
VI-7313c	256 C T	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTCTTAAAT TGTTTTGCAGTCTTTTATGTTTTATTATCATAGGTATAGGTGGACCTAAATTCCTATCATATCTTATT AATTCAGCCAGTGTATCCACAGTTTTTGTGTTATGTTTTAAGTAACCTATTATCTCTGGATTTCATG AAGGTGTAATATCGTTTTTGTAACTGAATAGAATTGTATAGCGATGA

NI-9281	68	G A	---	---	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCCTTGCTGGCTACTGG [G/A]GTGTTAGTTGCAGTCTGTGTCTCCCTCTCTTATGACTGTGTCC
WI-7848	142	A G	CTC	CAATTTATTTTG TAAACCCGT GACA	TTCTGAAAATATAACCCAGCATTTAGCTATTTAAACCTGTAAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACATAAAACAATTAATGCTAACACCTTTTAA ACCGTCTC[G/G]TGCTGAATAGCTTCAAAATAAATGTGAATGGT
WI-9304	70	G A	ACTGA	CCCCACAGAAC TATTGTAAAC AA	TCACGTTTGGTGTCTCAGATTCTGAGGAAATGCTTTGTATTGTATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTCTGTGGGGCTGTTTTTTGT
WI-7933b	314	C A	---	---	TTACAGAAACTTGGCCTGTGCTGTCCCATGCTAGGGGGGAGGGTCTTTTCCTTCTTCTTCC TACCTACCCCTTTTCTCTTGGCCAGGGCCTCGTATCCTACCTTTCCCTGGCTGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCTGCTGGGAGGAGGACCATAGCTCCCT
WI-7933	96	G C	---	---	TTACAGAAACTTGGCCTGTGCTGTCCCATGCTAGGGGGGAGGGTCTTTTCCTTCTTCTTCC TACCTACCCCTTTTCTCTTGGCCAGGG[G/C]CTGTATCTACCTTTCCCTGGCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCTGCTGGGAGGAGGACCATAGCT
WI-7374	182	T A	---	---	CCCAGATGTGCCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAACTGAAA CCATGGTGAGAAAGTTGACTTTGTAAATATTTGAAATGAAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTTGAAGAAATATATTG[A/C]AGAAACACAAAGGCTT GAT
NI-9343	78	C T	CCTCTGCCA	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGTACCTTGACCCCTCCCTTTCCCTCTGCTTCTCCTCATCATCATTCCTCAACAACAT CCTCTGCCA[C/T]ACACAACAACGTAAGTTTCAATTTGGCAAA
NI-7386b	104	T A	---	---	CTATATGTGAGAGGGGTGATATCTGGATGGAGTTGGGCTGGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAATTTGTTA[A/G]TGTTTGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
VI-9357	75	A G	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTAAACCTTCATGAAACCTGAAGAGTTCACTTTTGTATTAT GCTCTT[A/G]GTATTACAGACTGATGCCAGACAACCTTGGGAAGA
VI-9360	79	T C	TTGG	CCTTAGAAAA TCTGCTTTAAC A	TGAAGGGGTGTGGCACTGTGTTTCTGATGCTTACTACAATATGTGAACCACTACTTTAGAAAACTGTG CTTTAACTTGGT[C/J]ATTCTCTAATTGTGTTCCCTAGGAAATGACTGTCCCAAG
VI-7423	107	T C	GTTC	GGTCCAGAAGA GGCCG	TGCTCCCTGTCCCATCTGCAGTGGACCCCGACCCCTTTGAGGAGGTGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCATTGCTGGCTGTGTTCC[C/J]CGGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTGGGAGGGTGGTGAATAAAGGCATACTGTCT

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA A AAA	TGCAAAAGAAA GAATGAAAAGTT G	CCAGGAGCACTAGAGAGGGGGGAAGAGCAGAGATTAGAGAAAAAGCCAGGAGGAAAGG AAAAACATCGGCCAACCTAGAAACGTTTTCATTCGTCATTCCTCAAGAGAGAGAGGAAAGAAAAA T/AJACAACTTTCATCTCTTGCACGTTTCATAAACATTCACATA
X86400	118 A C			TCCTGCAAGAAGTTCTCAAGCCTTTTGATTTTGCAATAAAGTACAGCTTTCGATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTAATTTTAAAGTGAGA/CJTCCTTTTAAACACCT GTTAAATTAATGTAGCAGCTGTGAGAAATCTAAAAATATGTACCACTCGTTTATTTGTTTCATTCATCCA TCCCTTTCCCATGAATATTCA
WI-8053	242 T A			GTGGCCACTAGATGTTATAGAAACCATCATCTTGTACACAGCAGCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAAAGCATTAAAAAGTGTCCTCCATTTAAAGGGACTTTTAAATCAACCTAA TAAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAGGGTCCACA ATTAATCTTTGATCTTTTACTCACTGTAACTTATATAA/T/AJTCAGAAC
NI-6190	165 G A			TACACAATGAATGCTTTTATTTGGTATGCATCCACATTTACGCAATTTAGTGGTCTGAAACAGCAAG TGAAAGACGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACCGG GTTCTCTTAATCCCTGCTGAGGATCTT[G/A]GAAGCAGCAGCAGCACCAAAACCAAGGCATGCA CCGATTCAAGGTCTTTTGTCCAGTTGTCAGATTCCAACTAGACCCCA
NI-6275	148 G C			AACAGTCACCACCAACCATGACAACCTGCCAGGCAAGGCCTTGCTTCCCTCCCTCTTGCCTCC ATGTGCTAGTCAGCAAGGTGGGGAGGCACCGATGTAGCTTCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAA[G/C]GGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTCAGTAACCTGGTATGCTGAA
NI-6421	41 G T			ACCAAGAGATCAGCTGTCTAACACAGCAGCTTTTGTGATTG[G/TT]GGGCTTCTGTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACAAAA GAATATTTGGGGCAGAACCTGGAACCTGGCCACCAAGGACATCCCAATATCCCTCCTCCTCAGGG CTACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
NI-6905	215 T A			GGGTGAGACGGGTTTATTGTGCACATTTACACAGCGTCACAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGGTCGGGCTGCTACAAAGGCGTTCACCTTTCTTCCACACACTATGTACAGTCAGTGCTCCAA GGTGATGGGCTACAGTGTGTCATCAGTGAGTGTGTACACACATTTTACATAAATTACACACGACTC ATACATGAAAAA/T/AJAGAGCTAAGGGCTGTATTTAATGAGAAAAAA
WI-9420	202 G A			AACTGTTTACAAAAATAGGCTTTGCAAACTTCATTACTGAATTTGTAAGTCAATGACTGTGTTGTTT TAAATATGTACCAAGGAAATACAAATTTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACCTGCACAAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG [G/A]GCATTTCTTCACCTTAAGTGCAGCTGTGCAAGATGCCTCAGTGTG

NI-9448	184	GA ---	---	TGGGGCTGCTTTTAGACTTCATTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTGGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTTCTAAA TCCTGGCTTGGATTTAICCAAGCGCATGTTCTCAACGTGCCGTGAGGAG
WI-9470	204	GA ---	---	ATGTCAGAAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCCGAGATTCCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAGGGCTCACCTTCCCAAG
NI-1245b	201	GT ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	TC ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGT GGTTAATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	GA ---	---	TTCAAGTATAAGGACAGGTCTAGAACAAAGCGTTCCCAACCCTGGCACCATGACAGTTTGGACCAAA TAACCTTTTGTTCAGGGGACTGTCTACACATTTGTGGGATGTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCCAACAAATCATGACAAATGAAAATGTCITTAGACATT GCCAAATATACCTTGTGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	GA ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAAATGGTGACTCCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTAACATATGGTTTCTTCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCITTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	TG ---	---	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCAACCCCACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCAATAATAATGCTACAAATTTCCAGTAGTTACCAAGGCACAGCCTAT TGAAGAAATCATAAATGTAAACCTACAAATGATTGCTCTCTGCTTGTGTCAGGCATAGAGTT[G/]GGCCTACAAACCCATTTATCATTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	GA ---	---	TGGTATTTTTCCTTTCCCTAAAATGTTATGATTAATTAGTGTCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACACAGAAAGAAATAAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGAA[G/A]AGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAGTTAAGT

1-5801a	48 A G ---			TGGTATTTTCCTTTTCTAAATGTTATGATTAATTAGTGTCTTTGT/G/GAAATTTGAAAAAATGT AAATCAGAGAACAGAAAAATAAAGTATAGTTGAAACCTCTAAACAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
1-5696	61 C A ---			TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACCGAGGACAATGTTCAAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAACTGGGACCACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTATTTAACTT
1-7461	153 C T ---			TATTACTAGGTTTCATAGAGCCCCGTTGTATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAACGCTCCTCACTCCCTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTCTG TGGCAGGACTGTGTCT[C/T]GTTCCCTGTTGGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
1-9716	221 G A ---			AGAAGACAGGAGCAGCTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTGGTACTTCTCTTCTGAAGACCAACCCCTTCAAACCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCTTACATCTCGAAACCTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAAAATCTAGAA[G/A]AAAAACACCTAATTGGCTCATCTTGGATCA
1-9760	49 C T ---			TTTTCGTTAAGTCTTGTGAAGCCACACAGAGTGTACTCTCTTTAC[C/T]AAGTGTTACTTTGCA TATATTTATGGGGATGATTCTATCCCTACTTAAGATTCTCTCTCAGGTAAATATCCATTTCCCT TTGTTCAAGGAGTTCTTATTTGGCCTTCTTTCTAAACCCCTTAACCATCTGCTTATTCCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
1-9855	31 A C ---			GAAAACTCGTTGGCTCAAAGGAACTGTAGI/C/JAAATTCCTTTTATTTTGTGTTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGTGATGGCAGCTGCTCTTTTGTGTTGGTAAATCCTCTAGT GGGCACCTTGC AAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAAG TAGCAATGGAAGAAAGGTTAATGGA
1-10312	41 A G ---			AAGCCCCAGTGGGAAAAGCAGACAAAAACACTCCAAGAAATACI/G/JAGATATAAAACATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGGCATGTCAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTGTCTGGTGAGTCTGCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAAACTGAGGTAGAGTCACAGAGAAATTTCA
1-11152	179 C T ---			GATTCCTTGCAGCATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCCAGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCA[C/T]CTGTGCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

11-1968	167 A G ---	---	TTGTGAGGAGCTGTAAAGCTGAAAGAAATAGTCTCTGCTGGTCTTTGGTGGAAATGGATGAGTCTCTTTACAAAATTTTCCCTCTGCCATGGGTGTTATGTTTAGAATCATGGAGTTGGAAGACTTAGATTCAATTTGGGGCTGTACAGTTTACTGGAAGTTGT[A/G]TGAACCTTGAGCAAGTGTCTCTTAATGTCTCTCA
VI-4701	198 G A ---	---	GCCTCAATGCCCTTCCCTGTAA GGGTTCATTTAACAGCCTTCCCACCTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAGAAAAATGGTGCCACTATTGACTTGATAACACCTACAAAACAACACATTAACCTCTCCCACTCTACCCGCAAAAGTCTACCTTTTGGTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A]CCATGTCATTTTTCAGAAAAGCAGTATA
VI-4823	164 C A ---	---	TTTATCTTTCCAAACCATTGTGTGTTTCTTCACATACTTACGTAATTTAAATCATGTCAATTAATTAATGCACTTACTTGTGGCTACAGACATTGCTTCCCAATTTGTAATTCCTTAACAACAGCAAGCATAACTGATGTGCCATCTTTGTATTCCTAAA[C/A]AAAGAAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGTCTTCCCTGTTTCACCTCCCTGATTTCCCTATTCAGCATTCAATGATTA
VI-4860	72 A G ---	---	AAAAAACAACCTTCATTTGACATTTCTAAGAAAGATAAAGAAAAACAACGATCCACTGTGTGTTTGCTTGATTT[A/G]GGAGATAAACCTGATCTCTAAGAAAAATTAACCAAGCAGTACACTAAAAATAGCCTTTGTGTGTGGTTTTCAGGAAAGAAAGCCAATCCAATAAGTTGCTAAGAAAAATATGTTTCATATCACTCTAACTTCCACATAGAGCATTAAATAGCA
MI-9705	111 C A ---	---	TGAAGGACCAGTTCGAATGCCCTACCAAGGTAAAGTAAATCGGAGGGGCGAGGAAGTAGGAGTTGCTTCCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAAATTTGTTAACACTGATGCTGTCTACAAACGCACATAGAAATCGGTGTAGATTGCGGTCTCTAGTAAGTAGCTAATGTTTAGATA
NGR-4004Z48	177 A G ---	---	TGATTGTTGAATTAATTGTTGCTGTGTTCTTGGTG CAATAATCTCTGCTTAGAAAGTTGCTCTAGGGCCCATGGATTTCATGTAAGGGTGGGCGAGGGTGGACTGAAGATCTGTTGGCAGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCATCTTGGGCAATACGGTTATCCCGTGTCTTCATACGCCACAGA[A/G]TCTCCAAATTCAGGGGCTCCC
J17579	34 T G ---	---	GTGGGATGGTGGAGCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG GGGATTCAATGTGTCTCTCATCCAAATAAGCACT[G/C]CATGACCTCAGCCCCCATCTCTTCTCCC TATGTTCCCAAGAGACAGAAATAGACCTGGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATAGTGTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGATT[G/A]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTTGTGTTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTAAATAAGTATATAATTTTTTATGTTTTGTTCTGA

VI-7747a	44 T C ---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTTCTGGCCTGCT/CJTTCGTTAACTGIGTATGATAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAGTT ATTCTTGTTGTTTGGTATCCTGCCAGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCAATTTGTAATAAAGTATATAATTTTTATGTTTGTCTCTGA
VI-7189	197 T C ---	---	TCCAGAAATTTCCCTTCAGCTCAATTTTGCTCTCTCACAAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCAATTTTCCCTTCAACAAATAATATTTTACAGAAGCAGGAGCAAAATATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGTTATTTTATTAAGCCTACAACATTTTTC/JAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
VI-7850	57 G A ---	---	AGCCCCAGCTGGACTCATGGATGTGACCCCTTTGCTCCCTGCTCTTTCTGCCCTCTGG[G/A]CTCATGTA TCTGGCAGCTCTGTACCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTTGAAGCT GAGAGGCACAGGCAAGGAGCCAAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGCTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGCTGTCTACTAGAGCC
II-7907	69 G C ---	---	CTCTCTCTTCATCCCATCCCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAAGAGGTTGGGAGGAGG G/G/CJAGAAAGTGAAGGAAGATAGGAAGATATTACCTCTCTGTTATTTTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCCCTAATTTATATCTATAAATATATTAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAAAATTTATGTCAAAAGTTTAAAT
II-7919	242 T C ---	---	GAAGGCAGCTGGATCATTCCCGCAGTCTTGGGCAGCGCTTTGCTGTGGAAACACGAGAGCTCCTCCT CAGGGCCTGGCACTCACCTCTATTCTGTATGATGATTTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTTAGATTTTCTTACCCTAATCTGTTTAAATTTGTAACCTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAT/CJACAACTTT
II-7928	101 T G ---	---	CTCCCTTCCTATGTCTCAGCAGCACGTTGGGCACACTTGTTCATCTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCAGACATCGTCAAAATTCAT/GJACAAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCAGTGATGTTTGCACCTTAAAACTGAAATTCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCATTAAAAAATACGTACATTTTCGAGGTAATGGTA
II-7936	131 T A ---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATTTATATACATACTGCACTTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAAC[T/A] ACTGAATGAAGAAGTATTTGGTAACCAGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
VI-7944	99 T C ---	---	TACACGTTCCAGCCCGTTGCCCACTCATCTGCGCGCTTGTCTTTGGTGGGGGCGAGATTGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATGT/CJAGCCCCAAAGTACAGCCTGGACCCCTGGTGTG TGTAAGTAGTAAGATTACCTGAGCTGAGCTGAGCCTGAGCCATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGGCAATGCAATTGAACTAAGAGCTCTCAAGTCA

NI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGATGATTTTTTATAAATATTTTACATCTTTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTTGAATATGTGTG/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTGTGGAATAGTTTAAACAGTCAAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCTGTGTACTTACTTGGCCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGGCAGTGCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTGGCAATGTGCATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGGCTTTGCAGAGGAAAAATAGATTTCAATTGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAAGTGAATGCAAGTTGTACCAGTAAAGTTTATA TCTTCCATTGAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAATGTGTCTGTTGTTGTCATTGGCATTCTCTC/
WI-198	218 C T ---			GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCACC CATGATGGAACCTCTTGCCATGGTTTAGTACCCTGGACCAAGTAGTATCCATCCTGACTTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTCTCAGCTA CCTGCTTCCCTTTCTC/TGTTTAAACAAAGCATAGATATCTGAAACAAC
WI-205c	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG/T/CJCCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAACACTGCATATGCCCTTTATTTTGTAGTCCC
WI-205b	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAAAGCCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG/T/CJCCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAACACTGCATATGCCCTTTATTTTGTAGTCCC
WI-234	165 G C ---			GAAGACTGAGTTTCCAGGAGGTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNCCTTCCAGAGGCTCTCAGACTACCTCCTCCATCCTCCCT CTCCCCCACAACACAAAATACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGGTGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGCTTAGTTTCTCAATGGGAAATGG
NI-276b	25 A G ---			AGCTTTTGAATCCAAAACACAT/[A/G]CTTGACTCTCTTATCCTCCTCTGTTGTAAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTCTGCCGTGAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCCTCCTGCTATCCCTGATGACTGGGCAA

WI-276	25 A G ---			AGCTTTGAAATCCAAAACCACATAGJCTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCCTGAACGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTCTGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTAICTCTCTTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---			TTTTCCCAATCCACAGGTAAACATAATATGGATGTATAGAATTTAGAACTACTTCCG/AJGTTT TTTCCCTGGGAAATATTACAAAACATTTGTGGTCTGCAATCAGGTTAAAAGACATAGTGTGCCA TTTGTCAATCAGACAGGTAGAGCCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAATTTATAGAGCCAGGGCTTGCTCTGTGACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---			CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAAACCAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---			CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAAACCAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---			CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCAAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTTTTATTAAAAA AAAGNTATCTAAAGAGAAAACCAATAATCTCTCAGGTAATTATGGCCACAGCCAAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/AJGTAATGACCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/AJGTAATGACCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---			GTGTAATTTGGTGGCTTTGCAACTTTTCCACAGTAACCTTTAGAATNTNAAAGGTGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATGATGATGATAATGACCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATATTCTTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT

NI-611	66 G C ---			TTCAAAATTTACACCAATTGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGTCCTTGACGTATTACGTATTCGATCAGTCACCCATCTGGA ACCAAGGTTTTCATTTCTGCTGACCCCTCCCTCCTACCCCTACTTGGGCTCTGACTTCTTCTCTGGGCT GAACCTTCTCTGTGTGGCTGCTCGGCTTCTCTGCTTGGGCTCCCAATAC
NI-681b	156 A G ---			TGAAGCCCTCTCTCTATACCCCAAGTGCTTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACCTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCAACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
NI-681	156 A G ---			TGAAGCCCTCTCTCTATACCCCAAGTGCTTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTCATACAGGGGAAGCACCTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACCTATGGCACCATTGGGACACAGATTATATGTCAGA CACCAACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCATGGTTT
WI-867b	119 G A ---			AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTGTGTGTTGGC CAAATAATATCTCCCGAGGACGCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
WI-867	113 A G ---			AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTC[G/CTCCGTTTGIGTGTGGC CAAATAATATCTCCCGAGGACGCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
NI-867	119 G A ---			AATCTTAACAGCCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGAGCCTAAGATCAGTG CAACCCCTCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTGTGTGTTGGC CAAATAATATCTCCCGAGGACGCTCTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
VI-871b	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATGTCATATAA
II-871	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAGGTACCACAAATGTAACCTTGTCCTCAAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATGTCATATAA

884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTGCTGGGAAATCCATTTTGGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCCCTGATCTATTGGGA ACTTCTCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCGCGATGCAACATTTATTCACTGAGAAACATGATGAAATGAACATAAT
921b	205 G A ---	---	CACITCCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGACAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCTCTCAGCGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
921	205 G A ---	---	CACITCCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGACAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATCTGG CAGTGATGCCTCTCAGCGCTGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
945c	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTTGCTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
945b	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTGTTGCTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCCAAGGCCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
960b	167 C T ---	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTCTTCAGCAACCTAAAATGTTTTTGGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTCCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT[C/T]CTAGAGGTATAAGTATATAGGCATATTCT ATGATACTAAAGGTGGTATGGCATAAGAGTACATA
960a	155 G A ---	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTCTTCAGCAACCTAAAATGTTTTTGGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAAATGAGTGTTCCTACC CTGAGGAATTTATCAAAGATG/A]TTAAGTTATCTCTTAGAGGTATAAGTATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
1121	181 T C ---	---	TCCCACTGAGTATGGCTTCAGTAGTTTATTATGATGTCCTAGGTACATTTGTTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATGCTCTGACCCCTTTCTGTGTTCTG CTTCTAAAGATACAAAATAAATGTAACATTAGACCTCTCAGTAT[C/G]CTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAAATNTG

VI-1147b	204 GA ---	---	---	TTGCCATTATTTGAAGATAACCCACACACCTTGGTGCCAGGGTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACGCAAACTTCTCCTCCCTGCTGGCTC CTGAGCCAAAACAGGCAATTAACCAATAATCACTTTGTTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
VI-1158b	147 CT ---	---	---	GCATTAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCAGTGTCTGAATG/C/GGCCAGGT TAAGTGTGGGG/C/TJCTGGGGTCAGGCTGCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
VI-1158a	124 CG ---	---	---	GCATTAGAGGGTTCGTTTAAATGACATTCACTGAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTGTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
VI-1304	124 TC ---	---	---	AAGTTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATG/T/CJGNCANT AAAAATGATTTGAAATGGGAATAAAGCCCTCCCTCTAATGATTGACAGTGTAGACCTTGCCCTAG GCC
VI-1305d	202 CT ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
VI-1305c	46 CT ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTC ACATCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNATATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
VI-1305b	153 TC ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNATATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
I-1305	202 CT ---	---	---	TTCTCAATTCCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTCCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

I-1306b	248	A G ---	---	TTTCTGCATTGGAATAGTTGACITCTATGAGNNNGCAATAATAATGGACAATCTTTGTNGNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTJAGJGC
I-1306	240	A G ---	---	TTTCTGCATTGGAATAGTTGACITCTATGAGNNNGCAATAATAATGGACAATCTTTGTNGNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAGTGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTJAGJTCCTCCTAGC
I-1307b	118	T C ---	---	GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACITTCCTCCTCAGTTCCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTGGGGGAGCAGTGGTGTAGGCAATJ/CJGTGAGATTGTCTTT CCTACCCCTCTTAAATGTATCTTNCATTAATATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
-1307	118	T C ---	---	GACAAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACITTCCTCCTCAGTTCCTCAAGTGGACA GATTTCTGCATTACTGCTGGGTGGGGGAGCAGTGGTGTAGGCAATJ/CJGTGAGATTGTCTTT CCTACCCCTCTTAAATGTATCTTNCATTAATATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
-1325b	169	T C ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCCTCTJ/CJACCCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
-1325	165	C T ---	---	GAGAGATGGCCAAAGACAAAGCAGAGGGAGAGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCCTCTJ/CJACCCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
-1327b	162	T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAGTCTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGAGCTGAGAGTCTGTJ/CJGAAAGTTGGGTAGCTACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
1327	175	C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAGCTGTGTAGTGAAGAGTCTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTGAGTNCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGAGCTGAGAGTCTGTGAAGTTGGGTAGTJ/CJGTACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136	GA	---			TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTTNTGNNNTCCCTTTTCNTTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTTNAATTAACCCAAAGC [GA]GGATTGATGGATCTGTTTATTTTCTGCTGCTTGAACAGCAGAGTCGCTCTGNGAGTNTG GTTTCAGGATTGCTCTGTTTCCCCAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192	GC	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATA
WI-1349d	264	CA	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349c	192	GC	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATA
WI-1349b	264	CA	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATATGAT
WI-1349	264	CA	---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTGCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAAGTGAAGGATAGTCTGAAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAATATGATAGAAATTTGGAAGTACTAGATTTCAGAAAAATATGAT
WI-1403b	57	CT	---			TGGTATTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTACATCAACATAATTCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTGT
WI-1403	58	T C	---			TGGTATTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/TT]CCGAA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTACATCAACATAATTCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCCAAAGTGCCAAAAAGGGTTGTATCTGATTGT

II-1417c	31 C T ---	---	CAGCCCGAAGAGATTCACGTGGAGAGATGTC/TTGGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTCGGAAGTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGCGGGTTGC AGCGAGGGCCCTTAGGTCGTATTAAATGTTTGGCTTTGTAGAAAAGTCGC
II-1417b	31 C T ---	---	CAGCCCGAAGAGATTCACGTGGAGAGATGTC/TTGGCCAGGGCGGCAGATGTGAGCCACGGG GGTGACAGCATGCCTGCTGGCATTGGAGGGCCCGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTCGGAAGTTAAGGGCTCGGCTTCAAAAGCTGGTCCGGTTTGAGCGGGTTGC AGCGAGGGCCCTTAGGTCGTATTAAATGTTTGGCTTTGTAGAAAAGTCGC
II-1729	172 A ---	---	CCATGAGCAACAGCATGTTCTACTCTGTGATGTGTATGTTAGGGGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAGAAATTTTCATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTCCGTTGGTACCTTCTCTCCACCATCACCTGTGTTTT
II-1732b	122 T C ---	---	TGCTTACTCTTTGTTCAATCCCACTTACATTTTGTAAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTC/ATTCAGTCT CTGCCACATGTCTAGTAAGTGTGAGTGATGGTGATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTTCATCATATTGGTAAGGTATTCATCATATTGGCTAAG
II-1732	114 C T ---	---	TGCTTACTCTTTGTTCAATCCCACTTACATTTTGTAAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTC/ATTCAGTCT CTGCCACATGTCTAGTAAGTGTGAGTGATGGTGATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTTCATCATATTGGTAAGGTATTCATCATATTGGCTAAG
I-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCAAAAGGTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACCTTGGTAAAGGTGCTGTTTCTGGCAAGAGTCAG TGGAGTGTCCGGGAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCACTGCTGACTGAG CTACATTCACCTTATGATCTCCAGCAGGTTCCTCCA
-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTAC/AGTACGGCCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCCACCATGAAGCTGGCAAGAACAAATTCCTAGGAAAGTACAATTAC TGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAAGAAATATCATAAAAAT
1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/AGTATAGGTAGGATGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAATATATCTACTAAAGCATGACTTCTAGAAAATTAATTAATCTTGTCTCTCAA GGAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA

VI-1803b	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGTAGGTAGGATGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTGTGCTCAA GGAAATGGGAATACCTATAATACAGCTTATTGAGGAAAATAACTGGAATCA
VI-1837b	112 C T ---	---	TTTACTGGGATTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC/C/TTCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGAAGTCTGGGAACGTTTAGCTTTCTGCTGTGGCT
VI-1837	112 C T ---	---	TTTACTGGGATTTTCATAGCTGATCATAAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC/C/TTCTGTCCCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGAAGTCTGGGAACGTTTAGCTTTCTGCTGTGGCT
VI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/TTGAGAATCTGAATATTCAGCACATACAAGTGTGACAACCCACTTGTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
VI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAATGTAGCTTCATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT/G/TTGAGAATCTGAATATTCAGCACATACAAGTGTGACAACCCACTTGTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
VI-1879b	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/C/TTCTGCNAAATAAACTCCCAAAA AAGTGTAGTCCACAGGGTTTAAATAGTTCTTTGTAATGAATTTCTGTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
VI-1879	110 C T ---	---	GGGCTCAGTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTACTCCCCCG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC/C/TTCTGCNAAATAAACTCCCAAAA AAGTGTAGTCCACAGGGTTTAAATAGTTCTTTGTAATGAATTTCTGTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
VI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTACAGCTGCAAAAGAGG/C/TTGCTCTGAGAGGT AAAGTGCCCTGCCCAACCGGCACAACTAGAGAGAGCCAAAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAACTGCCATGAGAAACCACTTTTCTTGTCTCC

II-1900	119 C T ---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAAGTCCCATGAGAAACCACTTTTCTTGCTCC
II-1943c	165 C T ---	ATTCAGTTTCACAGTGGGCACAGGATCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
VI-1943b	165 C T ---	ATTCAGTTTCACAGTGGGCACAGGATCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
VI-1943	164 C T ---	ATTCAGTTTCACAGTGGGCACAGGATCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCCAATGGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCACGTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
MI-1960c	270 A T ---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTGGAGTGAGGATCTGGAGAAGCACCCCT GCAGAGCTTCATCTGTTTCAAAAGTGTGCCATGCANGTCTGGTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAATGCACCTCCCAACTT
MI-1960b	270 A T ---	CCAGGTGAGGCTGAAAGAAGGAAGGAGGCAATTGCTGTGGAGTGAGGATCTGGAGAAGCACCCCT GCAGAGCTTCATCTGTTTCAAAAGTGTGCCATGCANGTCTGGTGTGAGCTCATNGCTGAG TTATCAGAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAATGCACCTCCCAACTT
II-1977	203 T C ---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTTGTCTAGTCTGTAATAACTGTTGCCCTAGGAAGGTTGT TTCTCTAGTGTGTGAAAGCCTTCCCATCGAGTGTACAGTACTTCCAGTTATGGAGATTTT /C/TAAACATCAAACTGGCTGAGGCTGTTGG
I-2012	102 T C ---	AAATCTAGAAGCCAGAGTCAAGTCAAGTATTAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAACCTAGCTAAAAATC[T/C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGAAGCACTCAAAAGTTATGTAGAGTAGCTGCTCTGAGTCACTTTTTTCTACTCTCAT GGCTTCAACCAATGCTTCCACTGGATC

1-2013	127 C T ---		CTTTAGAGGTGGTCATTCGGTCCCTTCTGGAAAGTGATTGCTGTTTAAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACACTGACACTC/TCTCA CCAGAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGATATCTCAGCTTCTGAGCCCTGGTTACTGCAATCC
1-2032c	166 G A ---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACG/AJTGTTGGACCTCTGTCTCAACCTCCGACTTTTACAC AGATCATTTGGTTAGGCTCACCTTCTGTAATTGCTTCTGTTTTCAAAGGG
1-2032b	219 C G ---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTACACAGA TCAATGGTTAGGCTCA/C/GCTTCTGTAATTGCTTCTGTTTTCAAAGGG
1-2032	219 C G ---		ACCAGACATCCCATCAGGAGTTAGTCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTACACAGA TCAATGGTTAGGCTCA/C/GCTTCTGTAATTGCTTCTGTTTTCAAAGGG
1-2054b	188 C T ---		CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTATGGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTCTC/TCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
1-2054	183 T C ---		CGTTTCTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGTCTTTTGTGGTAGTTTGCT CAGAGCTGCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTTGGA TTTTATGGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTCTC/TCTGCTCCAC CAGCCCTATCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGTCTTT
2573d	129 T C ---		TGGGATTAACAAACCCTGTTTCTTCTCCAGTTACGTGCTTAAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTCCGTTTCAAGGTGTTCCGCTGTCTT/CJTGGA TATCATCTGATCTTCCCAACCAGGCTTATTTATGCTAGGTAGGGTAAAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG
2573c	165 A/C ---		TGGGATTAACAAACCCTGTTTCTTCTCCAGTTACGTGCTTAAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTCCGTTTCAAGGTGTTCCGCTGTCTTGTATAT CATCTGATCTTCCCAACCAGGCTTATTT/CJTGCTTAGGTAAAGGGTAAAGCAACAGAGGCTGTG TGAAGTGAATGATTTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG

VI-2573d	129 T C ---			TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTTCAAGGTTTCCGTGCTTT/CJTGA TATCATCTGATCTCCCAACAGGGCTTATTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG
VI-2573c	165 A C ---			TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTTCAAGGTTTCCGTGCTTTTGATAT CATCTGATCTCCCAACAGGGCTTATT/CJTGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG
VI-2573b	165 A C ---			TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTTCAAGGTTTCCGTGCTTTTGATAT CATCTGATCTCCCAACAGGGCTTATT/CJTGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG
I-2573a	129 T C ---			TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTTCAAGGTTTCCGTGCTTT/CJTGA TATCATCTGATCTCCCAACAGGGCTTATTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGGCTTGACGAG
I-2868b	60 A G ---			GACTTCATGCTCATGAACAAGCATTGTGCTTAATTTACAGACATTAAAGCAAGCTTCCJA/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGCTCTGCAAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
-2868	60 A G ---			GACTTCATGCTCATGAACAAGCATTGTGCTTAATTTACAGACATTAAAGCAAGCTTCCJA/GJCTC CCACTTCCCTCCCACTATCACCTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTAGGCTCTGCAAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTTATGGAACAGCTGAAAAATGAAATATCGATATAC
-2870b	131 T C ---			CATGCTGTGTAACCTCTGTGCTGTGCTGTCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATCTGAGGAGACAAGATGAACATCAGGAATGACTGGATAATGAIT/CJ AGAAATGAATAGAGCCCCCATTTAAATATATACAGCTTTATGTCCACTTCTCCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
-2870	131 T C ---			CATGCTGTGTAACCTCTGTGCTGTGCTGTCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATCTGAGGAGACAAGATGAACATCAGGAATGACTGGATAATGAIT/CJ AGAAATGAATAGAGCCCCCATTTAAATATATACAGCTTTATGTCCACTTCTCCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

VI-2954c	49 T A ---	---	TTAGCACATATCTGTGTGGGACTTAAGTGGGACATGAGACAAGGCATAAAAA[T/A]CAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
VI-2954b	41 A G ---	---	TTAGCACATATCTGTGTGGGACTTAAGTGGGACATGAGACAAGGC[A/G]TAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
VI-2954a	38 G T ---	---	TTAGCACATATCTGTGTGGGACTTAAGTGGGACATGAGACA[A/G]GCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
VI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACCTCCTCTCTTAATAAACCTAAC ATTCTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTATGATGTATGTCCTGATTTGCAATCCT AGTCTTTAATGTTATCTGAAGAAAACCTTTTACTAGGGATTGTCT ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACCTCCTCTCTTAATAAACCTAAC ATTCTCTTTGTTCCCTGACATCTGAAGGCCACGCTGTATGATGTATGTCCTGATTTGCAATCCT AGTCTTTAATGTTATCTGAAGAAAACCTTTTACTAGGGATTGTCT TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
I-2971	62 T C ---	---	TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
2995d	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
2995c	151 G C ---	---	TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
2995b	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

VI-2995c	151 GC ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
VI-2995d	133 A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTJA /JAAATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
VI-2995c	151 GC ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
VI-2995b	151 GC ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
VI-2995a	133 A T ---			TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTTJA /JAAATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
I-3147	85 CT ---			GTGGTGCAGTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCCAGCTTGAGACCCAG ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCCCTTACTCCTATCTCCTGAGACTTCTTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAAAATACITTTGCAAGG
-3234b	68 T C ---			ATTCTGTAATGTTTTTCACTGCTTCCAGTAAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAAACAACAAGAAAGCCCTCTGTTTGCAATCTGGCCTTTATAAATACCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNAATGAATCATTACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAAITTCAGAAGAAAGGACAAATGGAATGTACTATTTTINATATCTTAT
-3234	68 T C ---			ATTCTGTAATGTTTTTCACTGCTTCCAGTAAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA[T/C]GACAAGCAAGAAACAACAAGAAAGCCCTCTGTTTGCAATCTGGCCTTTATAAATACCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNAATGAATCATTACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAAITTCAGAAGAAAGGACAAATGGAATGTACTATTTTINATATCTTAT

WI-3292b	106 GA ---			<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC</p> <p>TCCCTGTCCCGTCCCAAGCCTATGTACTGGTATGCT[G/A]TGGTATTGGATTGGGATGGATTACTT</p> <p>GCCATGAATATTTCCATTGTTCTCATTATATGATTAATTAAGTAAATATTTATTTNCCATGA</p> <p>GACACAATGGAAAAATGGAAAAATTCATGGAAAAAACCCTTTCAATC</p>
WI-3292	106 GA ---			<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC</p> <p>TCCCTGTCCCGTCCCAAGCCTATGTACTGGTATGCT[G/A]TGGTATTGGATTGGGATGGATTACTT</p> <p>GCCATGAATATTTCCATTGTTCTCATTATATGATTAATTAAGTAAATATTTATTTNCCATGA</p> <p>GACACAATGGAAAAATGGAAAAATTCATGGAAAAAACCCTTTCAATC</p>
WI-3355	19 GC ---			<p>CCATGAACCATGGGCTACA[G/C]ATATTCCTAACTTCAGAGTCCCTCCTTACTGGAGAGGGATCCA</p> <p>CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCCTTCCAAGCATTAAACTCATCAGAA</p> <p>AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATACCTTCACCTTTTCAATGGAAAACTTTATAA</p> <p>ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG</p>
NI-3408	194 GA ---			<p>CCATGAAGAATGAGTTCCCTCCCTCCCTGGGTCACGCTAAGAATAGCACACCCCTTGAGAAATTNACT</p> <p>TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTCNAAGCTTT</p> <p>CTGGAATTGGGATGAATCTNACATTCATGTCACCCCTCGTGTGGATCACTTCTCC[G/A]TGCCCC</p> <p>ATCTCTGNGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAATCAGG</p>
NI-3505b	131 GA ---			<p>TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTATTT</p> <p>GAAAAATTGCCATTTTAAATATCTTTGGAACCTCCTAACACATTACCTATTTTNAACCAAAC[G/A]</p> <p>AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT</p> <p>GTTTAAATGGGAAATATGTTTGCATAT</p>
-3505	131 GA ---			<p>TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTATTT</p> <p>GAAAAATTGCCATTTTAAATATCTTTGGAACCTCCTAACACATTACCTATTTTNAACCAAAC[G/A]</p> <p>AGGTGATTCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT</p> <p>GTTTAAATGGGAAATATGTTTGCATAT</p>
3564b	177 CT ---			<p>GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT</p> <p>GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG</p> <p>TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTTC/TAACAAGTGTGTTGTTGTTGTCATC</p> <p>AGTGTACACATGCTACCTTCTTCCACAAAACAA</p>
3564	177 CT ---			<p>GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT</p> <p>GAAATCAATGTGCTTCCAGTGATTCACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG</p> <p>TGGGACTTCACTGGTTGACTAACGTTAACATGCATGTCTGTTC/TAACAAGTGTGTTGTTGTTGTCATC</p> <p>AGTGTACACATGCTACCTTCTTCCACAAAACAA</p>

VI-4230	93 T ---	---	---	AGAGACGTTGAATGGGGACATCTTTTCTATTTGATTTAGTTTAAACATTTGATAAGAAATGATGAAA GTTTGTCCACATTCAGATTTATCTTTATAGCAGCAGAAGTCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAGAAAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTCTGAAT ACATTTTAAATGGAGGAGAAATGAATAGTGACCTTTGAAATTTTGAATTTATGG
NI-4241	118 C T ---	---	---	GAAATTCATTGAAGTTTGGACCTTGAACCTGATCTCATTAATACATTTTNCCTGTAGTGGTTGATTT CATTTTGGACAACAGAAACAGACGAAATTTCCACTTAAATTAATTTCTC/TAAAGTATCTATGAT TTAGCACTGTTAGCACCAGAAACTGTGAAATTTATCTCTAGATATCTTCAGAACTCTAGGATGGAAG AA
NI-4271b	151 A ---	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCTTTGTCTCAGG CTCTTAGAAGGTCAGTCAGGGGG
NI-4271	151 A ---	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCTCCCTTTGTCTCAGG CTCTTAGAAGGTCAGTCAGGGGG
WI-4389b	156 G A ---	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACACACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATACCTTTGGA AGGTAAGATGTGAACCTATACA/G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGTATTGTAGGAACCTGGAAGCGGTAA
NI-4389	156 G A ---	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACACACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATACCTTTGGA AGGTAAGATGTGAACCTATACA/G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G ---	---	---	GATGACAATTATTGTGATTGGCATTTTAAAG/GGTACCATTCATTTCTCTGGCTTCGTGTGTT TGTTGTTGAGAAAGTCAGGGGTAGTCGTATTGCTCTTTCTAGTTCTTCTCAGTAGGAAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---	---	---	ACCATCAATGATACCTTCTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAAACCT GTCCTGGACATTGAAAAATAAACACATTACTATTGGTCAATTTCTGCTACTTACAAAGGTACTGCACTA AACAAAGTTAAG/G/C/GTTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACGTCA TTTCTTGCCCATAAATAAAATTTTACATGCGCT

VI-4584	144 A G ---	---	TTGGTTGGCATTAGCCTCATAACAACACTATTACAATCATAATTGTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTCTGCTTAGTCGCAGAGCCAGAAATTTGAACCCAGGAATCCATT CACCGGTACAGJTGCTACCTGGTAAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTGAANAATAGGTGTCCTTAAATTTGTTTATCAGTATGC
VI-4639	185 C T ---	---	TTTCTGCAATTTGAATGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCCJCTCATCTTTAAATTGTA AATTTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
VI-5327	63 A ---	---	AAATGAATCCGCTTTAGAGCAAAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA/A-- JGATTACTCATAAAAGCATATTAATTTTATAAATATGGAATAATTAACCTAGATAAATTAATGTGAAT TGAGTTTGAAGGTTCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNGCT TCAATAGAATGGCTCTTTCCGATGACAATGATGAACCTGTTCTAAGCAGACAG
NI-5390	87 C T ---	---	GCTTTTGAGAAATGAAAAGGGGAGCCCTGGACCATTGCAGGGCTCTCTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTATCTGCTGCTCTCCCTCTCTGGTATGCTTGTGTCATGAACAATGAATTC CCAGTGCCTGGCCGATTCTGGCTCCTAGAGGTGTCAGAAAAAAGTTCCGGTGAATAGAATTG ACGAATGGTTCAGAATTGAAACCTGGAATCTATGGAAGACAAACGAAT
NI-5404b	87 G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAGAAATCAATTATTAGCAGT GCAACATTATTTAATTTG/AJAAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAAAATTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTATAACAA
WI-5404	87 G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAGAAATCAATTATTAGCAGT GCAACATTATTTAATTTG/AJAAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAAAATTG AATCTTCTCTCAGCAGTTCCATGGTGTGAATCCACCCCATCTCTTTCCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTATAACAA
WI-5545b	77 A C ---	---	TAGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCCTC/A/CJCCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
WI-5545	77 A C ---	---	TAGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTCCACTCACACTGCCGCCA TATCTCCTC/A/CJCCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA

WI-5860b	134 A G ---	---	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTCTAAGATTTTATTGT TTCTTTTATATAAAATATGGAATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTACIA/ GJTTACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	ACTCAAGTTTGGGGGATAAAATCAGAAGTTTCTATGTACAACCTAAATTTTCTAAGATTTTATTGT TTCCTTTTATATAAAATATGGAATTTGTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTACIA/ GJTTACTGGAATCATGTGAAGACATTTCTAAAGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	GCAACAACCTATTATACCTGATTCACACCCAGGTCTACTAACATTAAATCAACCTAACCAACATAC TATATATTGTCCTGTTCTGAATTTATTTAGATCTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTTCCTCCAGGAGTCTCAATGTGAAGTATAATCTTACAGAG TAATT[C]GJATAGTAGGTCACCCACAAAGTCTATATTGTATGTGAAGGAAAG AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C]TGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C]TGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA AATGCCATACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[C]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGATTTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6109d	129 T C ---	---	GNAAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C]TGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C]TGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA AATGCCATACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[C]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGATTTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6109c	147 T C ---	---	GNAAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C]TGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C]TGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA AATGCCATACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[C]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGATTTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6109b	147 T C ---	---	GNAAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C]TGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATG TGNAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA AATGCCATACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[C]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGATTTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6109a	129 T C ---	---	GNAAAAATTATCCCTGAAAAATTTTATACCA AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCCCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGCTGTGTCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAAATTATCCCTGAAAAATTTTATACCA AATGCCATACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGA[C]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGATTTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96 T C ---	---	AGTGAACAGATTTGACTAAACATACCTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC

VI-6244	103	T C ---	---	---	TAATTGCACAACCTTACATATCAGGGTTCTGATTGAAAGGAAGAGAATATTCCTTTCTTTAGTGATT GCTTAATATTAAATTCATAAAGTGCACCATCTCTTC/GCTCCTTATAAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACAGGAGACATTTTATATACCTCTACAGTGGGGAAGACTT CCTATTTCTTTCCCAAGGATGGATACATTCTAC
VI-6268	124	C T ---	---	---	CTGGCCTTATAATCCAAGTTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCTCCTAGTAGGGCTTTGGGTGTGGCACCGTTGGCTCATTCTCTACTCTCCCT GGGTCTTATTGACTTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTCTTTGCAGAAAAGAGTCG GGGTCCAAAGATTTCGTACGATTTTATA
NI-6336b	234	C T ---	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAAATAGATCAGATGAAATGGACCATGTG GTACCCCAAGTGCAATTATGCTTGGTAGAGCCCTCTGAGGACACTGACAGT
WI-6336	234	C T ---	---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAAATAGATCAGATGAAATGGACCATGTG GTACCCCAAGTGCAATTATGCTTGGTAGAGCCCTCTGAGGACACTGACAGT
WI-6381	92	C A ---	---	---	TTGGATACAAAATTCAGTTACACAATCAGTAGCATTCAAAAATTTAGTTATGAGTATTTATACAATTA CAAAAATGNNTCATGTTTAAACAAC/CAGTATTTTAAAGCTCAAAACATTTTAAACAGGCACAAAT ATTCTAANGGCATATGCAATTCACCATGGCTTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTACAG
WI-6436	198	C G ---	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGGTTGATGTTGATGTTAGTAGGTTAGCGTT[C/ GIATTGGGTGTTATCCACAGACAAGGTGATGTTCTAAGATTTGATATTTATTGT
WI-6449	186	C T ---	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTCACTGCAATCTCTGATCTTATGCTGGCTCTATT[C/ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCTGTTGGTGTATTATA
WI-6449	186	C T ---	---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTACACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTCTATTCACTGCAATCTCTGATCTTATGCTGGCTCTATT[C/ATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAAATTTTCTGTTGGTGTATTATA

NI-6463	72 T C ---			GCTGGAGAGAAAGACCTCCAAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACATCTGAGAAAAAATTAAGTAGAACTCAAGAGGCCAAAAGTCCCAATTTGTCTCATTA TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCTCTCTCTC CAGTCCCATTTATGACATTCGGCATGCTG
NI-6474b	76 C T ---			AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---			AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGTCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCCACAGAGAAAAGGGGTGTTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---			GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCTGCTATATGCTTTATTTTGTA CACTGCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---			GAACTCAATTAACTTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCTGCTATATGCTTTATTTTGTA CACTGCTATTTACCTCCCAATAGTGGAGAAATCAGAGT[A/G]CTCCTTGTGCTGTTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---			CACATTTTGAATGCAACTGAGAAAANTGGTTTNTAGGCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA[G/A]TCAAAATTTTAAAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTCTGCTGAAATCTCAATTAATTTCTCCNCCATTCTCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTGTTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6564	54 G A ---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCTCTATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTCTGCTGAAATCTCAATTAATTTCTCCNCCATTCTCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTGTTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA

VI-6608b	46 C ---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAGGGAGGGGATTTCCCTAGTCCCTCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAGAACTGAACCTCCAGCACTAG GTAAAACTGCAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCAAGAAAAAGGAA AGC
VI-6608	46 C ---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAGGGAGGGGATTTCCCTAGTCCCTCCTCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAGAACTGAACCTCCAGCACTAG GTAAAACTGCAAAAAGAAAAACACCTGTGCCAGGCACTAGCTACAAGGCCACACCAAGAAAAAGGAA AGC
VI-6666	68 CA ---	---	GTTAGACAGTATCCAGCAAAAAGGTATTTTATACCTCTACTTTTCCAAAACGAGGAAACCTCCOC A[C/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATCTGTCTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCCTCTCTTCTCAAGTCCAGGCTTCTGGTAGACCAAAAACCTA ATACACAATGTTAGAGCACACAAGAGA
VI-6670b	120 A G ---	---	AGATTAAACATAATTATCTGGGGCCATTGTAGGGTNGGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/GJTTGTAGCCA GCATTGCCATTGAGGGCCGGAGTCAGGGTTGTGGGGCCAGAGTTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAATTGTAAACACAGACACAGAATCTTAGAAGGGAT
VI-6670	120 A G ---	---	AGATTAAACATAATTATCTGGGGCCATTGTAGGGTNGGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAAACCGTCTCAACAGTAAGCACACAATGAAC[A/GJTTGTAGCCA GCATTGCCATTGAGGGCCGGAGTCAGGGTTGTGGGGCCAGAGTTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAATTGTAAACACAGACACAGAATCTTAGAAGGGAT
NI-6704c	33 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT[C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
NI-6704b	33 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT[C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT[C/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGTTGTACATGTCATCATTAATCGATTCTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

NI-6710	106	G A ---	---	CCATGGACAGTTTAAATTAGGAAGCTTCGACTTGTAGATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACATTTTGTGAGGCTGGAATGATCCCG[G/A]TAGTAAACCTCAACATCCACACCT GCATAACATCGCTCCCAAGTGACTATTTATTAGTGCACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148	G C ---	---	AAACAAATGGTGCATTGCATAATAATTTGGTGCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATAATTATCACTGA GAATTTGGTCAACACAGTGGAGNGAACTACCCAAATCCAGTTCCCTTC
WI-6766	148	G C ---	---	AAACAAATGGTGCATTGCATAATAATTTGGTGCACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATAATTATCACTGA GAATTTGGTCAACACAGTGGAGNGAACTACCCAAATCCAGTTCCCTTC
WI-6787b	97	A G ---	---	ACAGATAAAGTCTTTATCCCTGTATGTTACATAAGAAAGTTCTTTACAGACTTTTATATACA ATCTTGTGCAGCAATGTTCAAATTTCAAGTACAGTATGATATCTTATGATCAACTGT ATGCTTTGTCTCTTTGGGAAGGACGGTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAGAGTAATTCAGGT
WI-6793	105	C G ---	---	GAACCCACAGTCTGTTATTTATTAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGTCTTCAAATCAATCAGTCAACCCCG[C/G]GAGTTAGAAAGTAGATCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGTTAATGCCCTTAATCCCCGAAAGGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37	T C ---	---	CACAATAATAAATCACTCCCTACCTGAAACCTTTAT[C/J]AGAAGCATTTTAAATTTACAACACA AAGCTCAACGACGNACCTACAATAAGTCTAGTAGTCTTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T C ---	---	CACAATAATAAATCACTCCCTACCTGAAACCTTTAT[C/J]AGAAGCATTTTAAATTTACAACACA AAGCTCAACGACGNACCTACAATAAGTCTAGTAGTCTTTACGNGCCAAAGGATAAGGCTGAACAATA AATTAACCCCTTTAAAAATGCTATGNACAAGTACAATTTCTTTTGTGAGTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTTGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAA[C/A]JTGTTGATACCTGTGTGCTCTACTNGCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTGTGTTCAAATCTTGGTTACGGTGGGCTGTGCGAG

WI-6817	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAAC[C/A]JTGTGGATACCCCTGTGTGCTCTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGCCTGTGGAG
WI-6819b	221 C ---	---	GATGGAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCAACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTG CTTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175 GT ---	---	GATGGAAGCCATTTATTTTCTCTAAATTTAAATAGAAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCAACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	GCAAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAACCTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAACCTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATAC ATGCAAAACCTTGTACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGTGCACGTG TAAGCTGAATTGCAATTTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATAATTCACCTAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C/J]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTCAGTGAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAATGGCAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153 G A ---	---	TTATAGAATACTTATGGGCATACGNGTAAATGAAGTGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTGGTTCGTCCTGAAATCCCTCCCTGCTCACAAAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGCAGGCAAACTTC[G/A]TAGAGCCATTCTGTGCAGAAGAGGGAAGGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGCGCTGTAGAACTGAGCTCATTA
WI-6909	73 C T ---	---	ATTGAAAACCTGTTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGAATGC AGACTTA[C/J]AAGCTTATAGAGAAAAGTCAAAAAGGAGCAAGTTTGTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCAACAGGATTATTTGGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTGTCATGCCCTAGTTGCTTATTTATACATATC

WI-6910b	163 G T ---	---	---	CACTCAAAACCTTTATTCAATTGATTACAAAGTGTACAATAATTTACAAAGTTAGGCATTATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACCTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCGACCTCCACGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	---	GCTTGTCTTTTGTGTTTGTGTTTAAAGTGACACCTTGGCCTGTGGGCAATTTCTTCACTTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAAACCCAGAAATGTGGTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTCTATTGTTAGTAGTATTTTTCAGATTTCCACAAAAGAACATG TATTGCTTTGTAAATTTGAAAAAATAACAACAGGATAGTAAAGATAT
WI-6928b	175 T C ---	---	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACCTTAAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACCTTAAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGG[T/C]AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A ---	---	---	TTTTATGAACATTTGAGATCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTCCCGNTAATTAAACTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAATTATGTGAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	---	TTTTATGAACATTTGAGATCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATTCCTCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTCCCGNTAATTAAACTATAGGTAGTATATTAAACAAAATGNGTTTTTNGCAATTATGTGAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---	---	---	AAACTAAAAACCCCTTATTGTCTCCAAGTGTGGGCAAAATAGAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACCTTAAGAAGCATTCAGTCAATAATACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCAATTTATGGCTGAAGAAGTGGATTGAAAACCACTTTAGG CTAAATAAATGATATGAATAATGCATAGACTGTGTATCTAGAAAAATCATGC
WI-6996c	242 G T ---	---	---	ACTTCTAGTGCCTGTACCACACCTTAATGCCCTCTGGTCGCCGACTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGGTCCCTCCCTCTGTCTTCAGCAOCCAGAGGAGAGCCGGCAGTCCCTG CAGGAGAGAGGAGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTTCTCTTCC[G/T]GTGGGATC

WI-6996b	242	G T ---	---	ACTTAGTGCCTCTGTTACCAACCACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCCTGATGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGAGCCGCGAGTTCCTG CAGGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCTCCGTCGTTGTCGGATC
WI-6996	228	T G ---	---	ACTTCTAGTGCCTCTGTTACCAACCACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCCTGATGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGGAGAGCCGCGAGTTCCTG CAGGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTTG/GCTCTCTCTCCGGTCGGATC
WI-7021b	112	G A ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAAGCCACAGACAATATGTTCCCAATG/AJCCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G ---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGAAAGCCACAGACAATATGTTCCCAATG/AJCCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTTCCGTTCCACATCCACACAGCCAATCCAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T ---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGACCTTGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/CJGGTGGGAGCCTCT GGGCTGTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTTGATA
WI-7056b	118	C T ---	---	GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGACCTTGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/CJGGTGGGAGCCTCT GGGCTGTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCAGCAGATGCCACATAAGGGGTTGCCATTTGATA
WI-7091b	153	A C ---	---	AATTCGCTGAAAAAGGAACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTTATACTGCTCTATAAATAGTATTCGAATCACTGTG CTTAATTTAAATAGCATT/A/CJCTTATCATTTATCAGCCTTTTATGTAATTTCCAAAGTAAAAATTA ACATATTATTTCATTGGTCTCTTTTATCTGGTCTATATGAATGCTAT
WI-7091	153	A C ---	---	AATTCGCTGAAAAAGGAACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTTATACTGCTCTATAAATAGTATTCGAATCACTGTG CTTAATTTAAATAGCATT/A/CJCTTATCATTTATCAGCCTTTTATGTAATTTCCAAAGTAAAAATTA ACATATTATTTCATTGGTCTCTTTTATCTGGTCTATATGAATGCTAT

[illegible]

II-7175	194	CT ---	---	CTCTAGACTAGTGCTTTACCTTTAATGAAGTGTGACAGGAGCCCAAGGCAGTGTCTCACCACATAAAGTTCAGAGAAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAACCATCAGTTACTGGTTTCAGTTGACAAAATATAATAGTTTACTGCTGCTATGTCCATGCCTA/C/TJAGATAATTTTGTATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
II-7178b	273	GA ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCACAGCTGCCTGGAGAGGGTCTCGCTGTCAGTGGCTGCTCTAGGGGAACAGACAGTACCCAGAAAAGCATAAACACCAATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCACCTAAATGAATCTCGTTCCCAAAGAACTACCCCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
VI-7178	273	GA ---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCACAGCTGCCTGGAGAGGGTCTCGCTGTCAGTGGCTGCTCTAGGGGAACAGACAGTACCCAGAAAAGCATAAACACCAATCCAGGGCTGGCTCTGCACCTAAGAGAAAATTCACCTAAATGAATCTCGTTCCCAAAGAACTACCCCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
VI-7182b	116	AC ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAGAAGGCTCAAGAAATTTATCACAGTTCCTCTGCAACCCACTGTGAGCC/T/CJCTCTCCTCTCTTTTACTTTGAGGCTGCCAATTACAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGGCCACTTGGTAGCAAGATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
VI-7182	106	CA ---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAGAAGGCTCAAGAAATTTATCACAGTTCCTCTGCAACCCACTGTGAGCC/T/CJCTCTGAGCCCTATCTCTCCTCTTTTACTTTGAGGCTGCCAATTACAGCCCCACGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGGCCACTTGGTAGCAAGATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
VI-7191b	273	TA ---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTATAAAGAGGGATAACAATGCTGATTACTACCTTTTAAATATTTAGATAAATGCACAGCACACAGCACACATCTAAGCAATTAGTGATGGGTAGCTGATGCAGCTTCATGTGGATTTAAGCACTCTAGAAAACAAATGAAGCTTCTTGGCATAATTTTAAGGAGCTCCCAAATGTGTACCTATTAAATGTAAGTCAAGTAGAAGACCATTT
VI-7199c	112	TC ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTCGCTTGGGTACCCACCGCTCTGCAGCTCCTTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGTTGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGGTCTGCTGAATTTCTCTTTATTATAGTCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGCTAA
VI-7199b	112	TC ---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTCCCTGTGGCCTTATGAGCTCAGCCTCGCTTGGGTACCCACCGCTCTGCAGCTCCTTGACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGTTGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTGTGGTCTGCTGAATTTCTCTTTATTATAGTCCCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGCTAA

WI-7216c	237 T C ---				TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCTCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCCCTGCTATACATAGGAAAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTGTTT[C]CTTGTAAATCACTT
WI-7216b	237 T C ---				TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCTCC AAGGACAAAATGTAGAAAGATGTAGATAACTTACTCAAGATTCCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTTCCCTGCTATACATAGGAAAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTGTTT[C]CTTGTAAATCACTT
WI-7220b	147 A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATATTGCTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAJATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7220	140 A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCATATTGCTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAJATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTGTTT
WI-7226	232 C ---				GATCGAATTTTTCAGATGATTCGGAAATTTTCATTCAGGTATTGTAATAGTGACATATATGTATA TACATATCACCTCCTATTCTCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTTTGATCATT CCCTTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACITCTTGGGGTTT
WI-7228b	254 G A ---				ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAGATATCTTTTGTGCCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAATAAGAAATGTTATCCAACTATTAAAGATATCTCAATGTT
WI-7228a	163 G A ---				ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTTCATAA TATGTTCCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAJGJAJATATCTTTTGTGCCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAATAAGAAATGTTATCCAACTATTAAAGATATCTCAAA
WI-7233c	213 C T ---				CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCCGGCTCTGTTGTACATCCATTTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACATAATATATTTAAAAATTTTCTAGGAAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGAAGTGAATA GTGTAAGTAJCTGTGCACAAACCCTGCCAGATAACCAGAGGGGCTG

VI-7233b	213 C T ---			CGATCGTACTGCCAGTAGCATTGTCTGTCTGCCGGTCTGTGTGTACATTCACATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACATAATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTGCCACCTTTTGTGGCAATATTAAGTGAAGTCTGCTAATA GTGTAAGTATC/TJGTGCACAAAAACCACTGCCAGATAACCCAGAGGGGCGCTG
VI-7233	211 T C ---			CGATCGTACTGCCAGTAGCATTGTCTGTCTGCCGGTCTGTGTGTACATTCACATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACATAATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTGCCACCTTTTGTGGCAATATTAAGTGAAGTCTGCTAATA GTGTAAGTATC/TJACGTGCACAAAAACCACTGCCAGATAACCCAGAGGGGCGCTG
NI-7238	128 T C ---			GCGTCTACAGACAGCTCACATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTCTT/CJCCGTT CTGTTTTAAACAGAAATAAAGGAGTGAAGCTCTTTCTCATTTCAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAACATTCAGTAGAACATTTATTGCGCTA
NI-7252f	520 T C ---			CCACAGGATCCAGCCCAAGCGGCCCTCCCGGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCCGGGCGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCCGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCCTGCGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
NI-7252e	552 T C ---			CCACAGGATCCAGCCCAAGCGGCCCTCCCGGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCCGGGCGCGCCAGCCCGGCCCTGGGCTCGGAGGCTGCCCCGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCCTGCGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
NI-7252d	540 T C ---			CCACAGGATCCAGCCCAAGCGGCCCTCCCGGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCCGGGCGCGCCAGCCCGGCCCTGGGCTCGGAGGCTGCCCCGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCCTGCGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7252c	552 T C ---			CCACAGGATCCAGCCCAAGCGGCCCTCCCGGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCCGGGCGCGCCAGCCCGGCCCTGGGCTCGGAGGCTGCCCCGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCCTGCGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7252b	540 T C ---			CCACAGGATCCAGCCCAAGCGGCCCTCCCGGCCCTTCCACTCGCAGACGCCGGGACAGAG GCCTGCCCGGGCGCGCCAGCCCGGCCCTGGGCTCGGAGGCTGCCCCGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCGCCCTAGAGCCCTGCGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA

NI-7252a	520 T C ---	---	CCACGAGATCCACAGCCCAAGCGGCCCTCCGGCCCTCCACTCGCAGCAGCGCCGGGACAGAG GCCTGCGCGGCGCCAGCCCGCCCTGGCTGGAGGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGCGAGCCCTAGAGCCTGCCCTGGAGCGTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTTGTTTATATTATGTAAAAATATAACGATCTCTT AAAAATACCACAGTTTGATTTTTTCTTTAAGGAGTAAAGATTTCCTTTT
WI-7265l	231 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTTGTTTATATTATGTAAAAATATAACGATCTCTT AAAAATACCACAGTTTGATTTTTTCTTTAAGGAGTAAAGATTTCCTT
WI-7265k	121 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTTGTTTATATTATGTAAAAATATAACGATCT CTTAAAAATACCACAGTTTGATTTTTTCTTTAAGGAGTAAAGATTTCCTT
WI-7265j	174 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTTGTTTATATTATGTAAAAATATAACGATCTCTT CTTAAAAATACCACAGTTTGATTTTTTCTTTAAGGAGTAAAGATTTCCTT
WI-7265i	227 T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTTGTTTATATTATGTAAAAATATAACGATCTCTT AAAAATACCACAGTTTGATTTTTTCTTTAAGGAGTAAAGATTTCCTT
WI-7265h	80 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTTGTTTATATTATGTAAAAATATAACGATCTCTT CTTAAAAATACCACAGTTTGATTTTTTCTTTAAGGAGTAAAGATTTCCTT
WI-7265g	170 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTTGTTTATATTATGTAAAAATATAACGATCTCTT CTTAAAAATACCACAGTTTGATTTTTTCTTTAAGGAGTAAAGATTTCCTT

NI-7265f	231	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AAGGAGTAAAGATTGCGCT
NI-7265e	227	T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTT/CCTTAAGGAGTAAAGATTGCGCT
WI-7265d	174	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGT/AJTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265c	170	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTT/GJTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265b	121	T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCAATTTTACCCATTCTGT/GJGGTTCATTGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265a	80	T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTT/AJTATTTGCCACCAAAAAGTAAATGCAATTTTACCCATTCTGTGGTTCATTGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7281b	183	C ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTCTGGCCAAAGTCTGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGCAGGCCGCGAG GTGTTGTGAAGACCACTGTTCTGTGGTGGGGTCTGCAAGAAGGCCCTCCTC
WI-7281	171	C A ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGAGCAGAGAGCCAAAGC ATCTCCCTGGGAAGTCTTCTGGCCAAAGTCTGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC/AJTGGCAAAAACGGAGTCCGCAGGCCGCG CAGGTGTTGTGAAGACCACTGTTCTGTGGTGGGGTCTGCAAGAAGGCCCT

I-7282b	159	G C ---	---			TGTCACCTGGCACATTCTTTCTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCACCTCAAAAATATGTCAACTTNNNNNNNNNT AGGCCCTTCATANAACCAAACT[G/C]TAGCAAGATGCAATGCATGGCAAACTCTGCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGCTGAGATTGG
I-7292	92	T C ---	---			CTTGATTACTTCACCTGAGGTGGGAGCATCTCCAGTGCTCCCAATATATCTCCCCACTCCACTAC TCTCTCCTCCACTTCATTTTCC[J/C]TTGTCCTTCTCTCTAATCAGTGTTTGGAGGCTGACTTGG GGGACAACTGATTATGATATTATGCTGTTTCCCTTCTTCCCAATAGAAGAATAAGTCATGGAGCC TGAAGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
I-7301f	133	A G ---	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG A/G]CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
I-7301e	94	T G ---	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/J]TGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
I-7301d	138	A G ---	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGT[A/G]TAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
I-7301c	211	A C ---	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]ATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
I-7301b	182	C T ---	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGT[G/J]CGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATT[A/C]TAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
I-7301	88	G T ---	---			AACTATGGCAGTGGTCTGTTATAGTAGAGGCGGGTATGGTGGTGACCAAGGATATGGAA ACCAAGGTGGTGATATGGT[G/J]CGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG

VI-7301	205 A C ---			AACATGGCAGTGGTCTGGTTATAGTAGAGGGGGTATGGTGGTGGTGGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGTTACATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTACITGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
NI-7314c	49 G A ---			CTCTCCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGGTCTTCTGTGCACTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAAACAAAACCTTGTTTTT
NI-7314b	49 G A ---			CTCTCCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/AJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGGTCTTCTGTGCACTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAAACAAAACCTTGTTTTT
WI-7314	36 A G ---			CTCTCCCTTTTCTTCAGATCTGCTCCTGGGTTTAA/GJTTGGGAGGTCA/GJTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCCTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGGTCTTCTGTGCACTATGAACGCTTCTTCCCAGGA CAGAAATGTGTAGTCTACCTTATTTTTTATTAAACAAAACCTTGTTTTT
WI-7321b	199 C T ---			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACTGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAAGNNNNNNNAGGTGGCACACCCCATC[C /TJTTTGTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---			ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACTGGCATGAGGAAG AAACAAGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGACTGCTTTGGCATCCAGGGCCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAAGNNNNNNNAGGTGGCACACCCCATC[C /TJTTTGTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---			AGACATTTCTCGTTCCCTGAAAGACTGAAGAAAGTGTAGTGCAATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCTCAGGCTACTATAGGTCCAGAAAGTCCATTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATCTGAATTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACCTTCATGGATCAGATCTGGGGCAGCAACCTATATAATCA/JA/CJA
WI-7338c	221 A G ---			CTCTTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTTCTTTACACAC/A/GJATACACACAGACATCAGAAATTTCTGTT

Jl-7338b	125	A C ---			CTCTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCCTGTT
	125	A C ---			CTCTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCCTGTT
Vl-7338	125	A C ---			CTCTTCTCAGCACATTGATGGGCAACTAGAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATATAAAATTCAAAGACTATCTGCAGCTA GTGTTGTTCTTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCCTGTT
	221	A G ---			CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAATACATTTGTTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
Nl-7384c	146	T A ---			CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAATACATTTGTTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
	146	T A ---			CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAATAACTTTAAAAATACCATTAATACATTTGTTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
Wl-7384b	145	T A ---			TGAAATCCTGGGTCTCTGGCCTGTCCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTTGTTGTTCCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATGG
	145	T A ---			TGAAATCCTGGGTCTCTGGCCTGTCCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTTGTTGTTCCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATGG
Wl-7388c	106	A T ---			TGAAATCCTGGGTCTCTGGCCTGTCCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTTGTTGTTCCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATGG
	106	A T ---			TGAAATCCTGGGTCTCTGGCCTGTCCTGTAGCTGGTTATTTTACTTTGCCCTCCACATTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTTGTTGTTCCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATGG

NI-7388	94	T A ---	---		TGAAATCCTGGGTCTCTGGCCTGTCTGTAGTGGTTATTTTACTTTGCCCCCTCCACACITTTTT TGAGATCCATCCTTTTATCAAGAAAGTT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAAGCATTGCAACAAGGTACCTCTATTTTGCACAAAGCGTCTGGGATTGIGTTTGA CTTGCTGTCTCCAAGAACTTTTCCCCAAAGATGTGTATAGTTATTGG
NI-7438	64	A G ---	---		TTAGATTTTAATTGGCAACCAAGCACTCACTGCCACCATCCACTGCAGATCTNCTATTCCTGG[A/G] GTTGATATGACAAGGAACCCCTATTGGAAACCAAGTCTTCAAGATTGTCAGATTGTCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTCACTGTAAACATAGTTTGTNCTGTGTTATTTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
NI-7454b	152	T C ---	---		CCATGATCCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152	T C ---	---		CCATGATCCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177	G C ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATCTATTTATAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTACCAACAATTAT
WI-7464b	168	C A ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATCTATTTATAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTACCAACAATTAT
WI-7464a	103	C A ---	---		AATTTGAAAATCTGAAAAAAGTGCATAAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAATGCATAAATCTATTTATAATTTCCCTAT GTACAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTACCAACAATTAT
WI-7499b	134	T G ---	---		CAATTCCTCAATCCAACTAGTCTGTNTGCCTAAACCATCCAGACAAACTCCACTTCGAAGGTTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGCTTCTTTGAATGCTTCAIT /GJTATAGTCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTTTTAGGA ACTCTGTACAAAAATCCCTTTTGAAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33	A G ---			CAATTCTCAATCCAACTAGTCTGNTGCCTAA[G]CCATTCCAGACAAACTTCCACTTCGAAGGTTTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCCTTTGAATGCTTCATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTAGGAACTCTGTACAAAAATCCCTTTGAAAAATATAAAATTTTGGAAATGAGTGATGA
WI-7506b	118	A C ---			TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAATGCATCCCAGCAGCAGACCACTTNAAGTAGTCTGGTGCTGATTGCCCTAGC[AC]GGAGAGTTGAGTGCCACAGGTAAGAAATGAGTGAAGAGGAAAAAATCATGATGTCATGATGCAGTAATTACTATGTCAGAAGAAAAATATTTAAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7506	118	A C ---			TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAATGCATCCCAGCAGCAGACCACTTNAAGTAGTCTGGTGCTGATTGCCCTAGC[AC]GGAGAGTTGAGTGCCACAGGTAAGAAATGAGTGAAGAGGAAAAAATCATGATGTCATGATGCAGTAATTACTATGTCAGAAGAAAAATATTTAAAAATATTGGACCACCTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143	C T ---			TGTGAATTCCTAGCTCTGGAAGGTGTTATGCCCTTGCGGGTTCTTGATGTGTCGCAGTGTCAACCCAGAGTCAGAACTGTACACATCCCAAAATTTGGTGCCGTGGAACACATTCOCGGTGATAGAAATTCCTAAATTGTC[CT]GTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTGCTAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135	T C ---			TGTGAATTCCTAGCTCTGGAAGGTGTTATGCCCTTGCGGGTTCTTGATGTGTCGCAGTGTCAACCCAGAGTCAGAACTGTACACATCCCAAAATTTGGTGCCGTGGAACACATTCOCGGTGATAGAAATTCCTAAATTGTC[CT]GTGAAATAGGTTAGAAATTTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGGAGAGTGTCTGCTAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162	G A ---			GGGAAAGAATAAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAAGTCTGTTTGACGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAACATAGATTGCATGCTTCCTCCTTCTCTT[GA]GGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTCTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162	G A ---			GGGAAAGAATAAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACCAAGTCTGTTTGACGGGAAGCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGTGACTTGAACATAGATTGCATGCTTCCTCCTTCTCTT[GA]GGAAGACCAGCTTGCAGTGACAGCTTGAGTGGGTTCTCTGCAGCCCTCAGATTATTTCTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60	T C ---			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC[CT]CTAAAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCATTCCTGTAAAGCCACTTGGGTCATAAAGAAGGGAAAGTAAAAAATGAAGTCTGACTAGAAAATCTATTGCAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGATATAGTTTTCATTTGATGTCATTTTGAATTTTCAG

NI-7555b	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGG[T/C]CTATAAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGCATTCCTGTTAAAGCCACTTGGGTCATAAAGAAAGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTTCAG
NI-7555	60 T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGG[T/C]CTATAAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTCGCATTCCTGTTAAAGCCACTTGGGTCATAAAGAAAGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGTATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTTCAG
WI-7567b	290 G T ---	---	TGAGCCATCACTAGAGAAAGCCCATTTTCAACTGCTTTGAAACTTGCCTGGGTCTGAGCATGATGGGAATAGGAGACAGGGTAGGAAAGGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGCCCTTGGATCGCTAAGCTGGCTCTGTTTGTATGCTATTTATGCAAGTTAGGTCATGATATTAGGATGGCCTACCTTTACAGGGICTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTCTGTT
WI-7569b	63 T C ---	---	AATGTAATCCCTTTCGGTCCAAACAGGAAACCTGACTGGGCGAGTGAAGGAAGGGATGGCAT[T/C]AGCGTTATGTGTAAACAAAGTATCTGTATGACAAACCCGGGATCGTTTGCAAGTAACTGAATCCCATGCGGACATTTGTGAAGGCTTAAATGAGTTTATGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTAAATATTGTATGAGTTCACATTGTATCATGCGCTACCCGAGGAGAAGAGGAGTTTG
WI-7574c	216 A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTGCCCTTTCCCTCTGTTTGTGTTGCCAAGGCCAAACGCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTGTACCACTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCCTTGATAGCCACAGGGC[A/G]TCTGCTGGCTGACCAACGTTACTCATCCCCGTTA
WI-7574b	216 A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTGCCCTTTCCCTCTGTTTGTGTTGCCAAGGCCAAACGCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTGTACCACTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCCTTGATAGCCACAGGGC[A/G]TCTGCTGGCTGACCAACGTTACTCATCCCCGTTA
WI-7574	216 A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGTGCCCTTTCCCTCTGTTTGTGTTGCCAAGGCCAAACGCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTGTACCACTTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCCTTGATAGCCACAGGGC[A/G]TCTGCTGGCTGACCAACGTTACTCATCCCCGTTA
WI-7576c	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGCCTTGGTTTCATCAGTGTTAAAAATTTTGAAGGGCGGTACTAGTTCAGACACITTTGGAAGTTTGTGTCTGTTTGTAAAAACTGGCATCTGACACAAAAAA[A/T]GTTGAAGGCCCTATTCTACATTTCACTAC

VI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAACAAGAAAAACATAAGAGAGC CTTGGTTTCATCAGTGTTAAAAAATTTTGAAGGGCGGTACTAGTTTCAGACACTTTTGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCTTATTCTACATTTACACCTAC TTTGTAGTGAGAGAGACAAGAACGCAANNNNNNNNNAAAAAGAAAAATAAAC
VI-7577q	77 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCA[T/C]CAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACAGTAGGAAGAAGAGAACATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTTATACATGACACTCTTCTGAAATTGACTGTATTTC
VI-7577p	50 G C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCAATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAAGTTCAATTTGGTTTACAC[G/A]TAGGAAGAAGAGAACATCAAAAGTGAGATATGTTAACT ATTGATAATGTGGCCTGTTTATACATGACACTCTTCTGAAATTGACTGTATTTC
NI-7577o	157 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAACATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTTATACATGACACTCTTCTGAAATTGACTGTATTTC
NI-7577n	48 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA TAAAAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAACATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATC[G/A]TCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAACATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577l	93 T C ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAACATCAAAAGTGAGATATGTTAACTAT TGTATAATGTGGCCTGTTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAACAGTAGGAGTTAATAA AGAAAGTTCAATTTGGTTTACACGTAGGAAGAAGAGAACATCAAAAGTGAGATATGTTAACT ATTGATAATGTGGCCTGTTTATACATGACACTCTTCTGAAATTGACTGTATTTC

VI-7577j	117	A G ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTA[G]ACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
VI-7577i	77	T C ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
NI-7577h	50	G C ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157	G A ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTACAC[G]ATAGGAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
NI-7577f	48	A G ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84	G A ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATC[G]ATCTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93	T C ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154	C A ---	---	AACCATGTTCCCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTATTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAGTTCAATTTGGTTA[C]AJACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

II-7577b	117	A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTATTACTTTCTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
VI-7577	107	G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAATCGTCTCTATTACTTTCTCTGAG/GJAGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
VI-7619q	106	C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
NI-7619p	150	T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
VI-7619o	228	A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCTCTCT CGCTTCTTCTTACACAGAAACAT/A/GJACATACCGAGAAACCTATTTC
NI-7619n	237	G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
NI-7619m	99	C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACAT TGGCAGGAAGATGGGGCTTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTTCTAAGGGGAGTGTGGGTCTGTCTCTCCCTTTTTCAT/AJCTTTTCCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90	C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C]/GJCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206	T G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGC[T]/GJTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106	C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150	T C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228	A G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTTACACAGAAACAT[A/G]CACATACCGAGAAACCTATTTC
WI-7619f	237	G C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99	C T ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACAT TGGCAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189	T A ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTC TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC

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VI-7619c	90 C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAAATACAGGAGAAAGCACAAGAC AGAGAAAGGGGCAATGGGTATCCGCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGCGAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCCTATTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
VI-7619b	206 T G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAAATACAGGAGAAAGCACAAGAC AGAGAAAGGGGCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCCTATTTTTCCTCTCT CGCT/GTCTTTCTTACACAGAAACATACATACCGAGAAACCTATTTC
MI-7619	189 T A ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCAAATACAGGAGAAAGCACAAGAC AGAGAAAGGGGCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCTCTAAGGGGAGTGGGGTCTGTCTCCCTTTTTCCTATTTTTCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
MI-7626d	105 A G ---			CCCTTTGTATGTGGAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCAGJTAAACCAATCATGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
MI-7626c	155 C T ---			CCCTTTGTATGTGGAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGACCAAAATGTGCA TACTAATGATGAGCAATTTAGCT/JACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
MI-7626b	281 T A ---			CCCTTTGTATGTGGAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGACCAAAATGTGCA CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
WI-7626	144 T C ---			CCCTTTGTATGTGGAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAATCATGACCAAAATGTGCA TACTAATGAT/JGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCTTTGGACTGTTC
WI-7689c	134 A G ---			TCCCATACCGCTGATCTCAGGGTCTCTGCTGCGCCGCCAGATGGGGGAAAGCAGAGTGGGC TTCCAGTGGGTGCTGCCAGGGCCAGACCTTTCTAGGACGCCACCCAGCAAAAGTTGTTCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGTGGTGGCACAATAAATGGATTATTAGAATTCATATGAC

WI-7689b	134 A G ---	---	TCCATAACCCGCTGATTCACAGGTCTCTGCTGGCGCCCAACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAAAJA /GTTAAGGCAGAGTCACACTGGGCAGCTGATACAAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7689	121 GA ---	---	TCCATAACCCGCTGATTCACAGGTCTCTGCTGGCGCCCAACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTCTAA AATAAGGCAGAGTCACACTGGGCAGCTGATACAAAATTGCAGACTGTGTAAAAAGAGAGCTTAAT GATAATATTGTGGTGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7690	45 GA ---	---	TGGAGAACATTCAATCTTGCCGTCACTATTCAATCAATGAAGATTAG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCAACAGCATGGTAGTGGCAAGAGAGGTCAGAGTCTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTTCATCC
WI-7703b	164 TC ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGAAGTAAATTC/JGGTCTCTCACTGTTTATTTAACCTCTAAATTCCT TTCAATTTAGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 TC ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTC/JAAGTAAATGGTCTCTCACTGTTTATTTAACCTCTAAATTCCT TTCAATTTAGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 CA ---	---	TTAATGAGTGTGTTTGTCAACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/C/AJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGTCTCTGGGCCCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 CT ---	---	TTAATGAGTGTGTTTGTCAACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/C/AJCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGTCTCTGGGCCCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAG
WI-7743e	106 CA ---	---	TTAATGAGTGTGTTTGTCAACCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC/C/AJCCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTCACTGGGTCTCTGGGCCCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC

WI-7743d	275 C T ---			TTAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106 C A ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAACTTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743c	106 C A ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAACTTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	106 C A ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAACTTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275 C T ---			TTAAATGAGTGTGTTGTACCCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGGAGCCAAAGG GTTACAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAACTTCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7758	144 A G ---			TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGTCTTCAGAGACTTCGTAAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[A/G]TAGTTTAAACTGCATTATAAATTTTATAACAGAAATTAAAGTAGATTTTAAAA GATAAAATGTAAATTTTGTATTATTTTCCCATTTGGACTGTAACTGACTGCC

NI-7765b	126 G C ---	ACAGGGCCCTTTGGCAGGTGCAGCCCCCACTGCCCTTGACCTGCCCTCCCTCATGCGAAATCCCT TCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGTGAGTATGG[G/C]TTAGG GAAACATTCCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTGCCACCCCTCATGCTGTGTG ACTCAACCAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTGCGA
NI-7773b	237 C G ---	TTAATTTACTGATTCAGCAAGACCAATCATTTGATCAGATTATTTAAAGTTTTATCCGTAGTTTT GATAAAGATTTCCTATTCCTTGTTCTGTGAGAACCTAATAAGTGTCTACTTTGCCATTAAGGCA GACTAGGGTTTCATGCTTTTACCCCTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTGACGTTTGACTAGCCATCTCAAGCAAC[G/TTTCGACGTTTGA
NI-7774b	170 T C ---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGACGGCACCCAGAAT CAGATCCAGCTTCGGCATTTGATCAGACCAACAGTGTCTTCCCGGGGAGGAAACACTTTTAA TTACCCCTTTTGAGGACCACTTTAATCTGTTT[C/JATACCTTGCTTATAATGAGCGACTTAA ATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165 G ---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACAATTTACCA TAATTTATTTTGCCATTGATGATTTATTTTGTAAATGTATCTTGGTGTGC
WI-7785b	165 G ---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAATTATTATCACAATTTACCA TAATTTATTTTGCCATTGATGATTTATTTTGTAAATGTATCTTGGTGTGC
II-7785	156 - T ---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGCTGTAAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANN /TJNNNNNNNGCCAAAGGCTAATCCAATTATTATCACAATTTACCATAATTTATTTGTCCATTGA TGTAATTTATTTGTAAATGTATCTTGGTG
II-7789c	84 G A ---	TCTCCCCCTCATCCAACCTCGAAAGTCTGAATCTCCCAAGGAGGCGCACCATCTTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
-7789b	84 G A ---	TCTCCCCCTCATCCAACCTCGAAAGTCTGAATCTCCCAAGGAGGCGCACCATCTTACAGAGACTCTCC TGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

II-7789	73 GA ---			TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGCCACCATCTTACAGAGACTCTCCC TGACG[G/A]JGGAAATTTAAGTTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
II-7790b	190 CT ---			AATTGTCAGTCACCTTCTTCAAAACCTTACAGTCTTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTCTTGAACCTC[G/T]TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
II-7790	190 CT ---			AATTGTCAGTCACCTTCTTCAAAACCTTACAGTCTTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTCTTGAACCTC[G/T]TCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
II-7795b	81 CA ---			CAGATGTTCTGGTAACTGATTGCTGGCAACAACAGATTCCTTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C/A]GTGTCATCATCAAGAAATTTAATGATTAATAAGCATGCCCTTCTCTCTCTCAT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAATTCCTTGGAGAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATCTG
I-7795	81 CA ---			CTTGATGATGAT[C/A]GTGTCATCATCAAGAAATTTAATGATTAATAAGCATGCCCTTCTCTCTCAT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAATTCCTTGGAGAAATGTCCAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAATATAATCTG
7814c	41 GA ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]JTTCATTTAGTCATGTGACCACTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTCTTAGAGAAGTATACATAAGTTAGGATAAAATATGGGATTTTC TTTTCTTTCTCTGGTAAATTGACTTGATATTTTAAAGAAATAACAGAA
7814b	41 GA ---			TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]JTTCATTTAGTCATGTGACCACTC TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTCTTAGAGAAGTATACATAAGTTAGGATAAAATATGGGATTTTC TTTTCTTTCTCTGGTAAATTGACTTGATATTTTAAAGAAATAACAGAA
314	28 GA ---			TGCTTGTTGTTCCACAGCCTGCAAGTTCAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAACTCTTAGAGAAGTATACATAAGTTAGGATAAAATATGGGATTTTC TTTTCTTTCTCTGGTAAATTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150	CT ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA
WI-7830c	54	GA ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA
WI-7830b	134	GA ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA G/AJATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA
WI-7830	44	A G ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA
WI-7865e	25	CT ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA
VI-7865d	191	CT ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA
VI-7865c	25	CT ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA
-7865b	191	CT ---	GCAGGAAATAGTCACTCATCCACTCCACATAAGGGGTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATAAAATTAATTTGTGTTCCCTTG AGGTGATCGTTGTTGTTGCTGCACITTTACTTTTTGCGGTGGA

NI-7865	25 C T ---	---	CCACTTCCTATCTGATTTTCCAG[C/TAATGAGGAGGCAATCTAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
NI-7865	191 C T ---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTCTTCCAACTGAAATCTCAATGTTCTCAGTAC/CTGAAAAAC CTGAATCACATGCCTATGTAAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	TTCAACACCTGTCTTCCACCCTCCACCATCTGTGCAATCACTTCAACCCTCAGCCTCAGTCCCO CTAACAAATACCCGTCAAGAGG[C/AGTGTCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCAATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ---	---	TTCAACACCTGTCTTCCACCCTCCACCATCTGTGCAATCACTTCAACCCTCAGCCTCAGTCCCO CTAACAAATACCCGTCAAGAGG[C/AGTGTCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCAATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTCCACCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTCCTGTCTTACCCCTATTCAAGCA[C/TTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTCCACCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTCCTGTCTTACCCCTATTCAAGCA[C/TTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868	66 T C ---	---	TTGATCGATCTTTCCACCCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGCTTT /CTCACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTCCTGTCTTACCCCTATTCAAGCACTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
NI-7870b	85 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGAATCCT[C/JATTTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAAATGAAATCCAATGAGCACTAGATAATTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACACTATTAATACTCTGCAGTGATTAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTTATCAGACTCTGTAATTGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTAAGCCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---			TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCGGGGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATGAAATGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
NI-7889b	54 C ---			TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGGGCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCGGGGGCCAGGGCCTCT GGCTCCCTGCCCAATCCTCCCTGGAGAAGGGACATGGGAATGAATGAAATGGGCGCTGGACACC TACAGCAGCAGCATGCTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7894c	142 A G ---			AGCCACCCCCAAATATAACTGTTATCCAGAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAAATTTGCAATTTTTATTGAAAAATTTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
NI-7894b	142 A G ---			AGCCACCCCCAAATATAACTGTTATCCAGAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAAAATTTGCAATTTTTATTGAAAAATTTATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
NI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACTGGCCATG[C/T]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCAAGTGAAA TATGATGTAATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC

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WI-7900d	128 C T ---			---	GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900e	84 C T ---			---	GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900d	128 C T ---			---	GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900c	84 C T ---			---	GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900b	128 C T ---			---	GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7900	84 C T ---			---	GCTCACTGTGACCCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAAGTTTGATCAAGCCATGGTGA[C/T]ACA AAATGCAATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAAGAAATC
WI-7901c	33 C T ---			---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACAACTCCAGGCCCTGGTTGGGGTCGCTGGTTATTGGGGCAGCGCCGTTGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T ---			---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACAACTCCAGGCCCTGGTTGGGGTCGCTGGTTATTGGGGCAGCGCCGTTGTCGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT

WI-7901	33 C T ---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATA[C]TAGACACACACAGGACACATATATAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTATATAAACATGGTAAGAC CCTTTTAAACAAACTCCAGGCCCTGGTTGCGGGTGGTGGTTATGGGCAGCGCCGTGGTGGT CACAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901	271 T G ---	---	AGACTTAGGTACAAATTGCTCCCTTTTATATAACAGACACACAGGACACATATATAACAGATT GTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTATATAAACATGGTAAGACCCT TTTAAACAAACTCCAGGCCCTGGTTGCGGGTGGTGGTTATGGGCAGCGCCGTGGTGGTGCAC TCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCTGIGT
WI-7926c	150 C A ---	---	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGACACT TTGGAGATCAGAAAAATTCATATTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCAIT TACAATGCAATACCTTA[C/A]ATTTTAACTCTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926b	28 A T ---	---	CATTCCGCATCTGTCAACCAGGACAGAAATJTGATGGACAAGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAAATTCATATTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTC ATTTACAATGCAATACCTTA[C/A]ATTTTAACTCTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926	150 C A ---	---	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGACACT TTGGAGATCAGAAAAATTCATATTAAGCAAAAGTGATACAAACACAGTGATTTGGGAATGCCCTTCAIT TACAATGCAATACCTTA[C/A]ATTTTAACTCTTGAGGAGAAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7947b	203 G T ---	---	AAGGCCAGCAGGTCAAAAAGGCCAACACACACCATAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCAGACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCTCAATTCAATCCATAGATTTGGAAGCCACA GA[G/J]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCATGCTGCCACCTG
WI-7947	203 G T ---	---	AAGGCCAGCAGGTCAAAAAGGCCAACACACACCATAGCAGCCAGACCCACAAAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCAGACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCTCAATTCAATCCATAGATTTGGAAGCCACA GA[G/J]TCTCTCCCTGGAGCAGCAGACTATGGGCAGCCCATGCTGCCACCTG
WI-7963b	145 T C ---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTAAAAATAAAATGCC ACAAATTTTCATTTCTCTCTAAGTATTACAATGGAGTTTATCTCTGCTTAAAGTGAAGAAAT TGAGTGAATGA[J/C]AATTTTGTAATTTAGGATAAGATCCAAAGTTATTTTCCCCAACTCTGTTCCTC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAGGCAGAGACGGGAAA

[illegible]

WI-8021b	57	C T ---			ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGTCCTTAGAACCTTCACCACAAGGAGTTTTCTTGTAGTGATCTCAAAGCTTGGTAGGCATTCGA ACTGGTCCCTTACATTTGAGATCTTTCTTTGCGCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTAATCGAATTCGGTGAATTGCCA
WI-8021	57	C T ---			ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGTCCTTAGAACCTTCACCACAAGGAGTTTTCTTGTAGTGATCTCAAAGCTTGGTAGGCATTCGA ACTGGTCCCTTACATTTGAGATCTTTCTTTGCGCCTCTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTAATCGAATTCGGTGAATTGCCA
WI-8024c	206	A G ---			CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGCGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACCACTTTACGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTCTAGTACACAAGGAAAAGAGC
WI-8024b	206	A G ---			CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGCGAGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACCACTTTACGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCGTCTAGTACACAAGGAAAAGAGC
WI-8077	167	A G ---			GAATGAGCCTTCCTAGCGCGAGGGACCTGCTGCTGTTGTTGGCTGCACATGCATCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTGCTGANNNNNNNNATCTGCCCAAACCTCTTCT AAGGAGTCTGGGTGTATGCCCTACAAACC[A/G]TAAATTTCTCATCAGATGGATTTTATTAAACGTT GTGATTGTGACTTACTTTCCAAATCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	G C ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAAATACAGAATGAGCTTGTTT[G/C]TTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAAAATACAGAATGAGCTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACTGGCAAAATACAGAATGAGCTTGTTT[G/T]TCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTTATTCCTTCCCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---	---	TCTAGGTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGA[C/T]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACCTGGCAAATACAGAATGTAGCTTGTTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---	---	TCTAGGTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAC[C/T]GGAACAATACAGAATGTAGCTTGTTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAATGGCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC[A/G]TGGCAGCAGGCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---	---	TTTTCTCTCCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAAGGGCAGGTGGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGTGTCCCAATAGAATTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACT
WI-8314	78 C G ---	---	GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCT[C/G]TAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTCTCTGTAGTCTTATGATGATCTAGAAGAGCAGTGTCCCAATAGAATTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACT

WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTAATTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTTCAGAAATG/AJAGTATCTTAGTATCTTCTA TTTGTCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTAATTTCAAGAGCTGCTGTATACTAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTTCAGAAATG/AJAGTATCTTAGTATCTTCTA TTTGTCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8332b	123	A C ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTCCCTGTCAGCCTTAGA/AJCJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCACTGTCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---	---	TATGTACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTCCCTGTCG/AJCJGCTTAGAAACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCACTGTCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCCTCCAACACGTTGGGG
WI-8378	308	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAAGGCGAAGG GGAAGCAAGGACCTTCTTCACATGGCAGCAGGAGAAAGAGAAAGGAGAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCCTCCAACACGTTGGGG
WI-8426	184	T G ---	---	TTTAGCACATATTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTCTCTTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACCTCGACTTGTGCCTAATAGGATTTGACCNNTAA GAGNNTCTTTGCTGTGGANGGGTGGCTTGTCTGAACTTCCATCTGTG/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGGCCCTTGGCNATNGNATTCAGTGAG
WI-8450h	61	C A ---	---	TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTCTATCTTAGTCCAAAGTTTGTGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAGA AAAAACCTTCCCAGTTATTGTGAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTCAAT

WI-8450g	55	T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAG AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108	T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCATTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125	T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCATTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125	T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCATTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108	T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61	C A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTCAC TCTTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55	T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60	A G	---	---	CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTACAAAAATACGTATTTTAAAGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGTACATTCGTACACACCACTACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAAGAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---			CTTCTCCTCCAAAATCTACATGAATACCTTGAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---			CTTCTCCTCCAAAATCTACATGAATACCTTGAGACAAATATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCAATTTTNNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---			CTTCTCCTCCAAAATCTACATGAATACCTTGAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---			CTTCTCCTCCAAAATCTACATGAATACCTTGAGACAAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A/T]NNNNNNNNCCCTTGCTTATTACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAACAACATTACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---			AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGGTAGTGACTTAATTTTGATAAAAAAAT TAAAAGCAT[A/G]AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATCTCCCTTTGTTTGTCTTTTAAAAACATTATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101 C T ---			ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAATCCCAGTCTGTCAGCTCAGTACCTGT[C/T]GTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTTAGAAAAACAGCCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTAACCTGTAAAAACAAG
WI-9439a	76 C T ---			ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAAT[C/T]CCAGTCTGTGAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCT GCCTGTAACCTTAGAAAAACAGCCCCCTACCCCCAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTTGTAACCTGTAAAAACAAG
WI-9446b	75 T C ---			GAAGGCTTGATTAAAGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[C/T]CCCTCTAAAGNACACATGCCCCAAATGACCANGNCATAGCAACACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTTGTNCCCTACTNTTATCACTGTGCTTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75 T C ---	---	GAAGGCTTGATTAGGGAGGNTTTATTGATGTGNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAATTC/CCTCTAAAGNGACACATGCCCAAATGACCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGTCNCCCTACTNTTATCACTGTGCTCTCTGCTCTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGTG
WI-9497b	185 A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATCTTTTTTT GAGATAATTATTCTAGATTCAGGCTTTCCTTAGATGTAAGTNCCTAAAGCTTATAGTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATTCACATGGAAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATCTTTTTTT GAGATAATTATTCTAGATTCAGGCTTTCCTTAGATGTAAGTNCCTAAAGCTTATAGTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAATTCACATGGAAAAGCCCAACAAAATAACTAAAACCTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAAGTTTCTATTTCATTCATCATAAGTATGCTAAGGATCATTTTGGAAAGATGTG CAGCATTCAGAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTAGCCATGATCTATGGTGATTTTCCACACATTTGTATC/AJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAAGTTTCTATTTCATTCATCATAAGTATGCTAAGTATGCTAAG[G/A]ATCATTTTGGAAAGAT GTGCAGCATTCAGAAGTTGTATCTCATCATGCGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTAGCCATGATCTATGGTGATTTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACACAAGTTTCATACATCACAAAAACCTTCCATTATAACACACAGAAGTGATTATACCAGAC AAGCATCAGTGATGTATCTGCTTTCCTTTCCTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GTT/C/GCTGGATACCCTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTCATATGTATGGATTTTCATAAACATTTATGATCCTTTTTTGAGGTAAGTAT AAATACCTTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATACATCTCAGATTAAAAATACAGGTAAGTATTTCAG GGNTAAATGGTACAAAAAGGCTGTAACTCTTTCCTTTCACATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGTACCATATATTTGTATCTNCTCTCTGGGAAAAACCTTTGGAAAAACACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTA/TGTGTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACACACTGACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCCTCTGGGAAAAACCTTGGAAAAAACAACACGCACA TAAGTATCATAAAGTGGGTTGGGACAAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTACTACTATACCTTTTTTCATCCTTTCA ACATCTTTTGTCACATTTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAGCT TACAACCTCTGTCTTTACCTGATACATTTATCCATTTACTTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGCTCTTTACAGATGCCCTGCTTTTATGTTAATTTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGAAG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTTA GGGTACCAAGGNTCTGAGTTGTAGTGTGTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTTGTTT

WI-9676h	134	C A ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCQ C/AJTTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT
WI-9676g	202	C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT
WI-9676f	184	G T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTTGGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT
WI-9676e	173	T C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTT/CJCCCTCTGTGCGCATGAAATAAATCTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT
WI-9676d	134	C A ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCCQ C/AJTTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT
WI-9676c	114	A G ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT
WI-9676b	92	C T ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT
WI-9676a	84	A C ---	---	GGCCACTGTCCAAAGTCTGCACAGTCTCCCATATGGCAAAGATGAAGAAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAAATCTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTAC/AJATTACAACCTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTGTCACTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGCTGTATTGCTGTCC
WI-9738	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTAC/AJATTACAACCTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTGTCACTTGCCTGGAGCGGGTGGTTTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGCTGTATTGCTGTCC
WI-9756	47	A ---	---	ACTGAAATGTAATGGCCAGGCCACCCAGGACCTTAAATCATAGAAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGCCCTTATCATTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAACACACAGATAATACACTTTTGGAAAG ATTTCCACTTAACCCTTGATTCTTCACTTTTTATGATTTAAACCTCCGTTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATCAAAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/A/GTAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAAACCGCTGGTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTTAAATCCAGGCAGCGGGGAAAAATGGATACCTTTTCATATGCTCTGTACCCAACTATAAATTTTG GTTCTCATGCACCAATTTTCATTTTGCCTTCTCACTCCAAGTACCAGTATTTTACCAATTTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTAGAATGTGGAAATTCCTATTACACACTTTGGCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCCTCCCTTTGCCCTCCTCATGCCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAATGCAGTTTC/AJTTGGATCCCACCCAGGA CTCAAAAACACTAGGAATTTGGAGAGAGGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATAIGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAATAATAC/AJGTGTGTATGTATATATCTTATTAAACACTT AGGATTATATACACACAATAAAACGCTCTGTAAAGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTGTTACTTGATATGCTGTG
WI-9880c	222	G A ---	---	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATTTGGCAGTTAACAATAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCCTGGACTATATAAGATCCCTTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA/AJTTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAAC TAACACCTTTCTTGCATGGATTTTCTTGAATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGAC/AJTATATAAGATCCTCTTTTAAAATTATATTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAAC TAACACCTTTCTTGCATGGATTTTCTTGAATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCCTCTTTTAAAATTATATTTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGAGGGCACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAACAAACGCCCCAGTTATCACAGTTCTNTTTTGTCTCACC ATTTCCATAACAAAAGAGCTACACAAAATTNGGGGGAGANACTCTCTTTGGAGACTGACACATTT TGCAGAGGGTGCATGAATAATGATTCCAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA/GJTGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATATTTATACATAAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTCTCTGGGTAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGAA/GJTGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATATTTATACATAAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAACGCTGAACCTTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAATTC/AJCAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNTATTTCTAAACCCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCCCTTCCCTTTTGGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGTACTTAGGAACCCCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCTCTGTACCAACATACATCGGGCCATTGGTTGATTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTC
S72904	51	G T ---	---	AGCATAGAAAAGTGATTTATATTTTAAATGGTTTCAAGTGGAAAGTCTCTTGTGTTAATTTGTGAGTTT ATTCCTGGAAATCTTTTGTAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAACCAAGTGTGTAACCTTCTCCCTCTCTGTCAATTTGGTTGCTCTTAAATA TTGCAAAAGTCTTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGAC[C/T]ACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANAAACAGTTTTCCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAAATAAACACAGCTAAGCTACTGACATAAAAAATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTTGGAAGTGG
ESTC129	20	---	---	---	AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAACTTCAGGAAAAATGAAACANGAGAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCGTCCICANAGICICICCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGACACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGGNGGGGCTGGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTGGTGCAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTTCCCTTGCAATGTTAGAAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTTTATTCATTTTAAATC AAAGANACCATTCATTTCTTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTAGCAGCATTTGG
ESTC146	20	---	---	---	CATGTCCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGCTACACAGACACTTAAGTACTGTATCGCTGTATGCGGCGCTGTGAGGCCCTG GGGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCATTTTTTTTCTTTTAAATACAAATCTACTGGTGCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACAGTNTTGCACGAATTATAAGTGGATCAACAAATT ATATTATTGATACAAACTCATGAGCATTTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCCTGGCTGCCCTGGGATGGAGCGGGGGCGGCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGCCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT
ESTC160	38	---	---	---	TTCTAGCATTGCTGTGCGAGTGGGGCCTGAGCTGGGNGCAGTCGGCAGTGTCACCTGGGCCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	CTCTTCGTCGGTTTGAAGTTGCTGTGTTTTCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAATATTGTTTTTGTAAACANCGAATACAATCCAATATATAACATTAAAAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAAATCANTTTGTCTGGATTAGAGGAAAGTGCCCGCTGTCTTCCATGACTT
ESTC176	23	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNCITTTATTTCTATTAATAACCTTTTAT TCTCTTTATTCCCATAAAAAGGCAACCAA
ESTC18	29	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTAAATATAATACATATTACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCTATTACGCTTG ATTTTACCTCA
ESTC187	24	---	---	---	ACCATGATTGCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG
ESTC188	25	---	---	---	TCTATTAAACAGGGTTATGTACACACCNTGTCAACCTTCAAACTCAAAACAGATGATACTCATCCTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAAATACCACITTTCCCTTAACCTTATCAGTCTAGTAAGCNTTTCAAAGGAGGAAAAATGGGTAC CTTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCTCCTCCCNCGCAAAGTCTCCACAAGCACA
ESTC20	33	---	---	---	AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNNGAACTCCAAGAATCTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	TCTTACTTGGGTAGTTTAGCAACAATTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGAGGAGGACAGACGCGGCGCTGGTGGCGCCCGAGAAAGGCTGGCGTGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	ACACTTAACAGGTTAAAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGA AAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCCAGAGTCCCTCCTCTCANACCAGGGCAGGAGGATTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTACACTAACAAAATTAATTAATCACAGGTATTNTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAATCTGCATGATTAAATAACATTAAACAAGTTCAT AAACACACCCCA
ESTC219	32	---	---	---	GTACACATCTGGGGTGAGCACACAGCAAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTAATTGNGAGAAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAAATACACANAACACACACACACACACACA
ESTC225	20	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	TTCTACTTTATTTTCATATTTCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	GCTTCCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAAGGGTTAGTCATATTCCCCANCAACAGCATGATAAAAAATTAATCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTTTCTCCTCTATTCTCTATAAAAAATAAAGGAAGCAGAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCCGGCCCTCAAATTCATATTTATCTTGAGCCGCTTGGTCAGGTTTGATTCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACAATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACATAACAAGCAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGNGGACCAGGGAACITCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTTATGCTGATGGAAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGCTGAGTTTGTCTTTGTAACNCTCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGGTGAGCCCTGCCGCTGTCCCATGGCCCCAGGAGCCACTGGTGCAGNCCGGGCAGATGTTTACCCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGCAGGAGGTGGCAGGAAGNAGTGGAGGGAAAGGACACCAAGT
ESTC57	20	---	---	---	AAGTGGCCCTCCCAGTCCCNCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAAATGATTTCCACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTTGGCTAGGCGTGGTTCTCATCTGTGAAATTTCCACAGCGCAATGACAGCANCCTCTCTCTCCCACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGGCCCCACGGGAGGGTGGGGAGACGACACTTTTCCCTGGGAAA
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGTCACTTTCCGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGCGCCAGATAGCTGTCTCTGAGTTGCANGCAGATGGAGATTTGGACACTG

ESTC72	37	---	---	---	GGGCTTCCAAAATGGGTATTGGGGCCAGGAGGCTGGCCTTTGGCGGTGACGCCTAAAAAGTGTGACC AACAAATTCACAGCTACAGGAAATCTAGAACAAAAATCAAATATTCATCACNITGGGTGAAAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACITTCCTGTCCCATCGGAAACCAGAGTTTCCCCAGNGAGCCCTTCCTATCTGCGGTTA
ESTC77	40	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGGTCTGAGATGTTCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC81	20	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGTATACCAAGTTTCCATAAANCTGTCTGTCTGGTGGGAGGCTACAGCCTGACCACATTC TTTGC
ESTC83	53	---	---	---	ATTGCAAAGGAAGTGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTTCCTTCGTCTTGGCATTCTGCTCTCTCCTCNGGCCAGTGTCCACCCAAGTGTCTTCCCAGTAT
ESTC89	22	---	---	---	CTCCCCCTCCTCAGTTCACAGTGAGACTANGGAGATTTCAGGGCAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCTCTCCAGAAGTTGNAGACGTCCTATTAGTTGATTATCTGTGC
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTC GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGAAGTGTCTTCCAC/TGCCAG ATTCTTATCAATGATCTTTCACCTAAGAACACGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATGCGATTITTCACAAAAATCAAAGAAAGAAAGGCTTAGCTG
DWU-100	127	CT	---	---	TTCCATCCTAGATATCTACTCAAATAATTGAGACAAGTGTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC/JG/GCCCCATTACAGTAGCCAAACGATGAAACAAACCCCAAGCTATATATTACCA GATGAAAGGATAAACAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGTATCCCTACTACACTGTGGAT
DWU-177	77	A	---	---	CAAAATCCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAAATCCAGCGGTGCCACCCAATCATGCCAGCTTCTGTATATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTCATGTCTGGGACTTACAATATCTCAAGGAACACGCAATG TCAACAGGG/JC/JGGGAAACCAGCCCTATCTGAGTCTTCGGCTCCCTCC
DWU-286	213	A	---	---	

EST10398 2a	147 C T ---			TGCTGGGTGGCAAGGCTGCAAAAGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAAACGGAAG CATTTGTTTCTTCTGTTGGCCAAAGAGGTATCTACCAATAGTGTCTATTAGGCATTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACTTCTTTT[C]CTCTTTAGAGTCTACCGG
ESTD- GPIK2L	38 G A ---			AGTCTCATCTGCGGTGCCAGGTAGATCCCTTTCAACC[G/A]CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCCCCGAGCAGCTGCTGGCACTGGACGGCGGCCAGGCTCACTCTATAGTGGGTCG TATTCGTCCACAA[A/G]TGATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGCTGCCCCGAGCAGCTGCTGGCACCTGGACGG[C/T]GGCGCCAGGCTCACCTCTATAGTGGG TCGTATTGTCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGCAGGAGGTGGGGAGGGGTCTGTCTGCCAGTCCCACAGACCAGAGAGCGGCTCAGTG TATCCCCACCCCCA[A/G]TGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCACTTTAA[A/G]AACTTTACCGGAGAGAAATTAATAATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAAACAGAAAGGAGGATGTAACA
EST36751 7	36 C T ---			CCAAGTCGTTCAATTTTAGCTTTCAGGTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTGCCCAAACCTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGATTAATAACAAAT[A/G]TTTACCTTTTGAACAAATAA ATGAAGATTGACCTGCTTGGCTGCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAAATACA GATGCTTCCCTTGTAGCAGTTTCAGCTCCTCTACCTA
EST18288 3	121 C T ---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCCCTGA[C/T]GGGAGCCAGT GTGACAGACACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAACCTCTCTGCTGGCTC TGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/T]TACAGCTGTGTTCTCATGGAGCAGGCTTCT GCTCATTCTGG
ESTD-ALB	180 A G ---			AATCCCAGCCTTTAGGAGGCTGAGGCAGGCATATCACAGAGTTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAACCCCCATCTCTACTAAAAATACAAATTAGCCAGGATGGTGTGCTGCTGCTGT AATCCCAGGAGGCTGAGGCAGGAGAAATGCTTGAACCTGGAGGCG[A/G]AGGTTGTGGTGAGCCGA GATGGCACCATTTGCACTCCAGCTGGGCAACAGAGTAAAAACTCTGCTCTC

EST70523 3	182 GT ---	---	TTCCGCCAGCCCCCATCTTGGCACCCCTGGTCCCCCTCAGGGGCCACCCCGGGCACTCACCGCTCT CGCTCTCGGTAACTCCGGCGGGCGCGCTCTTGGACATAGCTGACCGTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTCCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101 CT ---	---	CCAGGTGTTGTGGCACGTGCTGTATCCAGCTACTCGGAGACTGAGGATGAGATCTTTTGAAC CGGGAGGGCGGAGGTGCAGTGAGCTGACATGCTGCGCACTGCCTCCAGCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 CT ---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCAGATGAAGGCCAAATCCGAGAGACCTCTAGAGATACACGAGAC CGAATGTATCAAAATGGACATTCAGCAGGAATTCACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGACTCTTGTCTAAGAACTT
EST74167 6	137 C ---	---	AGACCATGAAGGAGTTGAAGCCTACAAATCGGAATCGGAACTGGAGGAACAACGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCAAGGAGCTGCAGGCGCGCAGGCCCGCTGGCGGCACATGGAGGA CGTGGCGGGCCGCTGGTGCAAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGC TGCGGGTGCGCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C ---	---	CGCTGTGTGCACTACCGGGGAGGTGAGGCAATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGCG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGCTCTCCGCGATGCCGATGACCTGCAGAAGCGCC TGGCAGTGTACAGCGCGGGCCCGCGAGGGCGCGGCGGCTCAGGCGCATCGGCGGCGGCTG GGGCGCTGTGGAACAGGGCGCGCTGCGGCGCGCACTGCGGCTG
ESTD- ARSB	126 A ---	---	GGAGAAATGGAGCCTGTGGGAAGGAGGCTCCGAGGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAACCACTCAGTGAA GGAAGCCCATCCCCCAGAAATGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144 C ---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTCAATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAT TCAACCTCCGATAGGGCTGGGCTGACCAAAATATACTGGTTTCTGTTCTCTTTCTGATCAT TCTTACAAGTTATACTCTTATTGGAAGGCCCTTAAAGAGGCTTATG
EST26021 1	137 A ---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCCTCTGCAGCACTTCACTACCAATGA GCATTAGCTACTTTTCAGAATTTGAAGGAGAAATGCATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTTCTTCTTTTGAACAAAGACAAAGCAAGCC
ESTD- BA511	29 A/G ---	---	GGCAACATAGTGAACCCCATCTCTACA/JA/JAATAACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGCTG CAGTGAGCCAAAGATGGTGCCACTGCA

ESTD- BCL2	116 A G ---	---	---	AGCTGGATTATAACTCCTCTCTCTCTGGGGGCGGTGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGCAGCTGGGAGAAC/A/GJGGGTACGACAAACCGGG AGATAGTGAAGTACATCCATTATAAGCTGTGCAGAGGGGCTACGAGTGGGATCGGGGAGATGT GGCGCGCGCGCCCGGGGGCGCCCGCCGCAACGGGCATCTTCTCTCCCA
ESTD-BCR	69 C T ---	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGAGACTCATCTGCGCAAGA GA/C/JCAAAGAGGTGAGTCTCTGTTGTCGGGAAAGGAGGAGGAGGTAACAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD- BRCA1aa	119 C T ---	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGTTTTCGAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA/C/JTGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACA GAACCAATAAAT
ESTD- BRCA1bb	139 A G ---	---	---	ACTAATGTAAGAAATCTGCTAGAGGAAACTTTGAGGAACATTTCATGTCACTGAAAGAGAA ATGGAAATGAGAACATTCGAAAGTACAGTACAGTACAGTACCAATTTAGCCGTAAATACATTAGAGAAATGTT TTTAAAG/A/GJAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCA GTATTAATGAAA
ESTD- BRCA1cc	126 A G ---	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGGTGAAATAAAGGAAGATAC TAGTTTTGCTGAAATGACATTAGGAAAGTTCTGCTGTTTTTAGCAAAAGCGTCCAGA/A/GJAGGA GAGCTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCAGAAAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST51212 0	122 A C ---	---	---	ATCCTGAGCTCGCCAAATAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCCAATTTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACA/A/CJAAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGCTGGGGATCCTCCTCCCTT/A/GJATTTGCTCCGGGAAGCACATTCA CAA
ESTD-C1R	40 A G ---	---	---	ACACAGGTGCTGGCACTGGGCTGGGGATCCTCCTCCCTT/A/GJATTTGCTCCGGGAAGCACATTCA CAA
ESTD-C6	31 A C ---	---	---	CCAGTCAGTTTGGGGACAGCCATGCACGTG/A/CJGCTCTGGTAGCCTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---	---	---	GTTCCGAATCCTCCTCTGAAAGTGGCCGGTTTAACTGCTCATGACGCTGCGGTGTGGTCCAGCT GAGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACCGGGTCTCTGGTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	67 A G ---	---	---	ACAATCCAGGTACACATTCAGAAAGAGAGGGGTGGTCAGTGAGCCTGGGTAGTCCAGTAATCCA A/GJGGATTAGGAAGGAGGCCACCGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T ---			GGCAAGTTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAAATGGGAGTGCCCAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAACATAATTGTCTTCATTATGGTCTTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---			TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACACAGACAGCT CTCAGAGCAACCCTAGCCCATTTACCTCTTCCCTTCCAGAGGACCTGAANAACGTGTTCCCAACCCGA GGTCGTGTGTTGAGCCATCAGAACGAGAGATCTCCACACCCAAA
ESTD- CB24	145 A ---			ACCAGGACACAGACGCTCTCAGAGCAACCCTAGCCCAATTACCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTGAGCCATCAGAACAGATCTCCACACCCAAAAG GCCACACTGGTATGCTGCGCCACAGGCTTCTACCCGACACGCTGGAGCTGGTGGTGAATGG GAAGGAGTGACAGTGGGTGAGCAGACACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---			GTTTTCTTTCAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCTTTTCTCTATCTTCGCCGT TCTGCTCTGAAACAGGGCATGGAGATCCACGACACAGGGCGTGAGGGCCAGAGCCACCTG TGCACAGGTA/GJCCTACATGCTCTGTTCTTGCAACAGAGCTTACCAGCAAGGGTCTGTCTGCCC ACCATCTCTATGAGATCTTGCTAGGAAGGCCACCTTGATGCCGTG
ESTD- CB27	125 C T ---			TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCTGGTGGATTTCAGGAGTGCTGTGGAGTCTGCTCATCACTGAC[C/T]TATCTTC TGATTTAGGGAAGCAGCATCCCTTGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTGTTTCATCTGATGGAAGTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---			TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATGGCAGGTATATGA/TATGTA TTTCTTAAACAATAAATGAAAGTCCAAAATTACTCTTGATCCATGGACTGCAGAATAAATGTTA TTTGTAGCTGTCAGAAAACAATACTAATCTTGCAATATGTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTCATGCAAGTAG
ESTD- CYP2D6	61 A G ---			CAGGCCAGCGTGGTGGTGACCATCCCGGCAGAGAACAGGTACGCCACCATATGC/AGJCA GGTTCATCATTTGAAGTGTCTCAGGGTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG AAAAAACATTTTAAACACCTTTTCAATCATATACACCATAT/ATTTTCCATTTTTCACATAAGTCA GTTGAGCTGAGTTTCCAAATTACTTGCAATCTAAATGTCAATACTGATTAAATGCAAGTTCAACAG ACAACTTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTATGCCCA TATCTGCAITGTC
ESTD- D1S1873	40 A C ---			CATCCCAAGCCCATCTTAGCCACTGGCATTTTGGCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGCGCCCTACCCCTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTGTGTGGCTATGTGGTGGTCTGTGTAGAG/C/TGGGGGCTTTGGTTTCAAGTTGCATTATGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- 17S33b	169 C T ---			

STD- J17S33a	75 C T ---	---	CATCCCCAAGCCCATCCTCTAGCCACTGGCAATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGCCCTTACCCCTTTGAGTCCATGGAAAGGCTCCTCTGGGCGG GTGGGTTGTGGCTATGTGGTCTGTGTAGACGGGCTTTGGTTTCAGTTGCACATTTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC TTTGAGACCACCCCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTG GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGGAGGAGAAATGCTTGAACCC[A /GJGGAGGCAGAGCTTGCAGTGAGCCAAGATCACACCACTGCACCTACAGCCTGGGTGACACAGTGA GACICIGICTCAA
STD- J18S8	133 A G ---	---	AACTGATTAGAACCTGAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACAATTGG AATTTTGCATCATTAAAAATCCAATAAAGTACACTGTAATAAAGAAATTTAACAGAATATCATTGT TTATCAAACATTTATCATTATTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCIA/GJGGAGCCTTGATGTCATTTCTGTATCTCCT CAGGTATCCCACTTGAGACGTACTTTTCAAAAACTCTACAGCCGTTGTTGTTATTAAATCAAGGT TGAACATAAAGTA
STD- J3S11	44 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTTCCC AGAAAGTGAACATACTGCTCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTACGATGG CAGGTATGAAATATAATAATCTGICCTTTATTGGAAGGATGCTGTTGGT
STD- J3S12	37 A G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTTCCC AGAAAGTGAACATACTGCTCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTACGATGG CAGGTATGAAATATAATAATCTGICCTTTATTGGAAGGATGCTGTTGGT
STD- J3S2a	248 G ---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCC[A/GJGTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAACATGACAAACATTTTC GTGGGACACCGAGGCTCCAGGCTGGCGCTTGACGCTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGAGACA GAATGCTGATT[A/CJCTGTGGAGAACCAAGAACTTCTGGCCTGTGGTAGGGCAGCTGCTTCCAAAG ACCTCTGATTGTAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT GTGGGACACCGAGGCTCCAGGCTGGCGCTTGACGCTGTGGCTCAAGCAGCTGCTCGGCCTCCA[C GJTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGAGGAGAGA CAGAACTGCTGATTATCTGTGGAGAACCAAGAACTTCTGGCCTGTGGTAGGGCAGCTGCTTCCAAAG CCTCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT
STD- J3S2b	247 C T ---	---	
STD- J3S2a	248 G ---	---	
STD- J3S399	83 A G ---	---	
STD-DMb	146 A C ---	---	
ID-DMa	66 C G ---	---	

ESTD- DRD1	154 C T ---			TCCCAGCCCTATCGGTCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAACCCATCAC ACAAACGGGTACGACCCCAACCTGAACCTGCAGATGAATCTCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGC/TCTGGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCCTTTGGTCAGGAGGCTGCCCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCCCGGAGAGGACCCGGTACAGCCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGAGCCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCGCCCAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCCAGAGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---			TCTTCAGGATCCGCATCTGCGCTGGTTGGGCATCGCTCCGCTAGGTGTCAGCGCTCCACCAGCTGG GGTGAGGGGTGGTGAGTGC/TGGGGCGCGGTGCAGACCCGCGGGCTGGGAGGACTTCA CCCCGCTCACTCCGTTTCTCGAGCAGTCTCCGTCGTACT
ESTD- ETS2	43 A G ---			ACTCAGAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCACCA/GJGGAAGCCGTCTGGGGCCTG GCAGTCCGTGGGACGGATGTTCTGGCTGTTGAGATTTCTCAAGGAGCGAGCATGCTGTGGACACA CACAGACTATTTTAGATTTCTTTGGCTTTTGCAACCAGGAACAGCAAAATGCAAAACTCTTTTGAG AGGGTAGGAGGTGGGAAGAAACCAACCATGTCTTTTCAAGATTGTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTCTCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTGTGAAGTATGATGTTTA/GJGTCAAACCTTCATTTTTTTTTTC ATAGGTATGTCCAATTTATCCAGCACAATTTGTTAAACAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGCACTCATGACAAATTTGAAGCTGACAATTACACAAGAAAGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTTGAACCTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAAT
ESTD- GODH	200 C G ---			CGCAGACCGGTGAGTGGGGTCCGGAGTGTGGAGGGAAGGAGGAACTGGGGTTTAGGGACT TTCCGGGTGACTTTCCCGTCTGTGCTTGAGAGAAAGGGGAGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGTCGACCGGTGTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGAGTTC/ GIGACTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	88 A G ---			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCAACCATGAC AACCACAGGCCCTCTCAGGA/GJACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCGAGCGCGCTGAGCCCAAGGGAAGCAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCCCGAGTCCACAG

EST34088 2	62 A T ---			GTGGGGCAACAGTGGAGAGAAGGGGCCAGGGTATAAAAGGGGCCCAAGAGACCGGCTC/A/T ACAGGTAAG GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC/A/GJGGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCCTAGG GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTACAGTTTGTCAGAGAGATAAAAGGATAACCTGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAAGACACACCTT AACACAAAGCCCCAGCGAGAATTGAACTCGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGAGCCCTCGTCTGCTGTTGGTTTCTTCTTCCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATCTCTCTACAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAGGTTCT CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCTCCCTTGA CTTTGAGTCAATTTGGCTGGACTTGAGTCCTGAAACAGCAAGAGAAAGAAAGG/A/GJCCCCAGA AATCAGAGTGGCAGCTCGCTACCGCATCTCCCTTCACGGGAATTTTCAGGGTAACT ACCCAGTGGAGCCCGCTCATTCACGGTCTTGGCAGGAGTGCTGTTGGGAGAAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC TTTACTATTCAATGGATACAGAATTGTGGGAGTCACTATAATCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTGCCTACATTGTGTGAGTGACGGGCGAGTGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGATACGAACTGAAAGT ATGTAATACTTCACAAATACTAATAACGGAGTTGAATATAAACCCCA CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCAATATTATTATTATTTATTTTTTGG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGAGTGCG/A/GJCAATCTGGCTCACTGCAAGCT CTGCCCTCTGGTTTCATGCCATCTCCTGCCCTCAGCTCCCGAGTAGCTGGGAATACAGGCCACCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTCAACCGT CCACTACAGATGGATAAATGGGTACAATGAAGGGCCATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTGCTGCT/A/GJGGAGCTCTGTCAATTGCAGG TCCAGGTGGCTGGACCCAGGCCAGCTCTGCAGCAGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGTGAGCCAGGGGCCCCAAGGAGGACCTGGCTTTCAGCCTGCTCAGCCCTGCTGCTGCTG/A TJCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGGCTCTGCCCCCTGCTGGCTGCTGGCC CTCTGGGGACCTGACCCAGCGCAGCCTTTGTGAACCAACACCTGTGGC
ESTD- GNAT2	56 A G ---			
ESTD-HT2	154 G ---			
ESTD-HT5	149 C ---			
EST37382 5	124 A G ---			
ESTD- IGFBP1	43 C T ---			
ESTD- IGHV4-6	120 C ---			
STD-IL1A	110 A G ---			
STD-IL1B	99 A G ---			
STD-IL1A	134 A T ---			

EST45311 0	151 C T ---				GCCCTCCCTCTCCAAATCTGTCCCTATAGTTTCTCTATTAGTGAACATACATGCATCTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TACCTCTTTCAITTAACAGCCCTTATCAATGGCCTTTTCTTTTCAGTA GTACATACACATCTGTGTCAATTTGTTGAAT
EST65258 8	80 A G ---				TGCCCCATCAGCGCGCGAGACATGGCTTGCCACAGCTCTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTTCQ/AGCCCTCAAAATGACAGCCATGGCCGGCGGTGCTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGCTCTTGCCATGGAGACTTGAGGAGGGAGGGCTTGAGGTTGGT GAGTTAGGTGGTGTCTCTGTGCAAGTCAGGACATCAGCTGATTAAA
EST38216 3	26 A T ---				ATGCAGGATGAAGGTGGACAGGGAGG/TJGAGGGCCAACTGTATCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149	G T ---				ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTTATAGCATTTGTTTAGCATTACCTAA TTTTTTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGAAG TTTTTTTCTCTG/TJAAGTGCCAGTATCCAGAGTTTGGTTTGAAGTGAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTGGGGTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- RT10a	133 A G ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCCTATTACTTCTAAG GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
STD- RT8b	231 C T ---				ACCTCACCCCTCCCTTAGCCCTGAGGAGGAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCGTCCTAGGTTTACCA/C/TJGTCAACATTGACACA
STD- RT8a	21 C T ---				ACCTCACCCCTCCCTTAGCC/C/TJGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCGTCCTAGGTTTACCA/C/TJGTCAACATTGACACA
STD- RT5099	82 C T ---				CACCTGTGTGTAGATCTCTCAGTGGCCGCTCTACTGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCA/C/TJGGGGGCAACCGGAAGACCATCTTGAGGATGAAAAGAGGCTGGCCACC CCTCTCCTTGGCCGCTCTTGAGGTGTGG

ESTD- LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATGTAACCGTAGCAAACTGCAATTGGTATTTAGA AAAATAAAAAATTTCCAATATGTAGTGTGTATACCTGCTCTGCCATGCAGCATATAGCCTGT GGGAACC/A/GGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG/A/CJACAGATTCTTGAAGACAGCAGCGGGATGGGGCAGGAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G ---	---	TACACACTTTCCTTACCCTTCACTGAAAACGACT/C/GJGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCTAGGGGCACCTCACCACTCCAGCTTCTTCAGCTCTGCCCTGTCTGCTGCTGCA AGGTTTGTCTTAATCTCAATTCATGTCTCTTCATCTTTAG/C/JAGCTGTGGGTTTGTGTTG TTCTCTGTTTTGCTTAGTATCTGACTACTTTTAAATTAATAAAGAGATGTATCTAAACAAAAATAG AGATTGTTATCAGAAGTTTCAACAATTTTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGTCCCTAGC/C/JGAACTTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGTCTTCCAAAGGTTTGGTCTAAGTTGCTGATTACC/C/JGGATTTTCTGACG ATCTTTCAACTGCTAGAGCATCTGTTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAATTA/GJACCAGATCCACAGACTGATATGGCTGGT AACATGGACTTGTATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTA/GJGCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTGTAGGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTCTTTTAAACCTCACCTTTGTGGGTTTGTGAGAGGTTATCA
ESTD- NFKB1	107 A G ---	---	TGTCCTTAGGCCAGCCCTGCTGTCTCCCTGGCTTATCTTC/A/GJGACTGCAAGAGAACACA GACAT
ESTD- NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGTTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGCTTGAATAGTAGTCTTATTTAACCTTGGCAATAGCATTTG C/TJATTCCCTGTGGTTTTTAATAAAAAAT
ESTD- NRAS	202 C T ---	---	GCACCAACACCCACCCAGCACACCTCCAACCTCAGCCAGACAAGGTTGTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGG/A/GJGTCAGCCGTGTATCATCGGAGCGCCGGG CACATGGCAGGGATGAGGAAAGACCAAGAGTCTCTGTGGGCCCAAGTCTCTAGACAGACAAAAACC TAGACAATCACGTGGCTGGCT
STD-PAI1	100 A G ---	---	

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCACCGAGTCTCTTACCAACACGAGCTTATTGCTGTCCGAGAGGTACAACCCGCTAGA ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTCTTCTGCTGTCTAGAACGTTTTCTTAG GACTGGCAGTTTAAGCTTTCACCTAGGCTTCTGTATACCATGCC
ESTD- Per/RDS	74 A G	---	---	ACCTACAGACGTCGCTGGATGGTGTCTCAACCCGAGGAATCTGAGAGCGAGACGAGGCTGGCTG CTGGAGA/G/GAGCGTGCCGGAGACCTGGAAGGCCT GGAAGAGATTTAAGAAAGCTTGATTGGG/C/TAATCTGGTCTTTGAGTGTGGAAGTTCATGTC TCTGCCCTGAGTTACAACAGAACTCTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAACTAGACTTTAAGGTAAAGTAAGAAAGTAGTATTTTTTA GGAATATTTAAAAATATTTAAAAATACCTCCATTTTGCTT/AGTCTCTTTAGTGAAGATGATACCTGC AAAAAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGGCTTGGAAITGGATTTTAAATGTTGACTTTATCAT
EST54045 6	39 A G	---	---	ATGAACATGTTCTTTAATTTATGATATGTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAA/G/GAGCGAGCTGTGTGACAAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAATCATGTTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTTAATCTT CCCGAGGAATCTGAGAGCGAGAGCGAGGCTGCTGTGGAGAAGAGCGTCCGAGACCTGGAAGG CCTTCTGGAGAGTGTGAAGAACTGGGCAAGGCAACAGGTGGAAGCCGAGGCGCAGACGCAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA TTGGGAAGTTAGAGCCTATATTAATTAACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAGTTGAAATGCTCAGTTC/GT/CTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
ESTD- PX/MP1	88 A G	---	---	ATCACAGGTCCTGTCTCTGGCCATCATTTCTGTGGAGAGATGG/A/C/TTGGTGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGAATGACATTGATGAGTGAAGATGTC/TTGGCTCAG GATGCCGGAAATGAC TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACC/C/TTGGTCTATACCTTTATCTATAGCCTT CCCCTAGTCTT TGAACACCCCTGTGGTCCGAGCCAGGTTGTGTTCTCCTGGAGCCCTGAGGAGTTGTTGTCTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCTGGACATACACCTTCACTCCCTTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCTGGCCTGTTGTGACAC/C/TTCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCCAAGCCAGTTTCTTAGCAAGGGCAGGAC
ESTD-RDS	127 A	---	---	
ESTD- S14544	94 G T	---	---	
EST52908 0	45 A C	---	---	
EST19590	55 C T	---	---	
EST76136	39 C T	---	---	
ESTD- SPTB	176 C T	---	---	

ESTD-TAT	224 C	---	---	---	AAATGGTCAGGACCCTGATCCACAAGAGTGGTACCAATTCATCAGGGCCATCAGTTCATTGAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCATTCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTGTTTACAACCTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	125 A C	---	---	---	TGCGGCTTTCTCCGGCAGGTAGACTTCTTACTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATC/A/C/CTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTGTTCCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTCA/G/TATCCCCAA GCAGTGCATCCATTGACACATAATATGCATCCAGACAAGAGGTCAATAATATTGATGTCGTAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGGTCCTATGGGATGACA AGTAGTGGATGAAGCTAACCCAGCTCTCTCACTGATCAGTATCAATGCTATGCTGAAGATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAAATGCCCTACTCTTATGCAATAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATGATTTCTTTCACCTTTATACCTTCTTCT AATACAAGCATATGTTAG/A/C/JATTAAAGTTCTAGGCATACCT AGTAGTGGATGAAGCTAACCCAGCTCTCTCACTGATCAGTATCAATGCTATGCTGAAGATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAAATGCCCTACTCTTATGCAATAGTATCACA AACCACCTGGTTGAATATAATAGATTGAGTTAATGATTTCTTTCACCTTTATACCTTCTTCT AATACAAGCATATGTTAG/A/C/JATTAAAGTTCTAGGCATACCT TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTCAAGAGACAGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD-TYR	122 GT	---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTCAAGAGACAGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- TYRP1	222 A C	---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTCAAGAGACAGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- TYRP1	222 A C	---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTCAAGAGACAGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 CT	---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTCAAGAGACAGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 CT	---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTCAAGAGACAGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G	---	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCCAAGACACAAGGTCAAGAGACAGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCCCGTTATATGACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607	105	A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTCTAGTATCATATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCAC/A/GTGGCGGGGATGGCCGGCGGGAGTTTC TGGTTGGCGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGAGGGGGGGTGCATGCCTGAGATGTAGATGCGGCC
ESTD-VWF	36	G --	---	AGGTAGGAAAAGCAAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTTGG TCCCCTAGAGTCTG
EST71770	189	C G ---	---	AGCACCACTCTCACGTCAAGCCTCAGCACAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAG[C/G]TGTGGTGGA AGGAGTCCCCAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
ESTD- TNFab	152	A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGTGTCCTCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTC/A/GJAATCGGAGCAGGAGGATGGGGAGTGTGAGGGTATCCTTGATG CTGTGTGTCCCCAACTTCCAAATCCCCCGCCCCGGATGG
ESTD- TNFaa	88	A --	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGTGTCCTCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTTACACACAAATCAGTCAGTG GCCCAGAAGACCCCTCAGATCGGAGCAGGAGGATGGGGAGTGTGAGGGTATCCTTGATGCTT GTGTGTCCCCAACTTCCAAATCCCCCGCCCCGGATGG
EST52418	113	A G ---	---	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCACTACCCCTTTGGTGGCTACAAGATGTGG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT/A/GJAAGTGAAGAACTGTGAGTG TGG
EST13586	89	A G ---	---	CCCACTCTATTGCCCAAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC/A/GJGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC
EST51976	123	A T ---	---	CCGGTCACTC AGGCAGAAACTGGCCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAAGACCTTCAAGGAGAAAGAGAGCCAGGACAAG/A/TCTCTCTC CTCCCTGAGCTGGAGCAACAGCAGGAAACAGCAGCAGGAGCAGCAGGAGCAGGAGGAGGAGGAGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCCCTGGTGC
EST11458	140	A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTGTTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC/A/GJTAAACAACTTCTATGAGCCAGGAGAAAGAGATTACGTTATCTCTGCAAGCCGGGCTATGTG TCCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCCCTCTCTGTAAAGGGAGTTTGTCTTGGATCTCCATGGGCCAGC[CT]AGCA CTGGTCCCTGTGAGTCTGTATCAGGTAGAGGATGGACCAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
EST39852 8	106 C G ---	---	CGGCTTCCTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTT[C]GJGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCTGGGGCCCGTGG TCCTCCTGGTGTGCTGGGTAGTCTCTGGAGTCAACGGTCTCTT[A]GJGTGAAGCTGGTCTGATGGCA ACCCTGGGAACGATGGTCCCAAGGTCCGATGGTCAACCCCGACACAAGGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	AGTGACTTCCAAGGAAATGGCTACCCAACCTGCCCTCATGCCCTGCTGGCCAACTATGCCCTCAGA ACATCACCTACCAC'TGCAAGAACAGCATTGCATACATGGATGAGGAGACTGG[A/C]AACCTGAAAA AGGCTGTCATTCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAATGTATATAGTCTCAAACCTGGCCATCTCCATTTTCACTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGTCACTTT[C]A/GJGGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTCTGGACCTGGAAACA[C/T]JGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAAGATATACAATACAATTTTATTTGACCAACACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGCAATGCCCCGGAGTTTCTCCAATGTGTGGAGAAGGCCCTTAGAAGACATGTTTGATGCCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAAAC TGGGAGGCCGGGCAT[A/G]GTGCTCATGCCCTGTAATCCCAAGCATTTTGAGAGGCTGAGGGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGTCTCCAATAGAGCCCTTACCAAAGTGTAT TACATAAAGAAGTCAAGTGGTTTTACTCCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGTGAGAACTGTTCTCTGTCACCATGGAGGATACTATAACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G -- ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTCTATCTCCAGCGGCCCTGTCTATC CAGTCACTCATCAATGGGGCCAGTCAAGGCCAGGCACTGGGCTCCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	TTTGGGTTGGATTGTTCTTTTGGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAGTTTGGCTTGGCTGCTGTGGGATATTTGAAAGAGATC/TJTTTGCCAGTCCAATGTCTCTAGAGATTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT
ESTD-FVR1	109 A G ---	---	TTGATTGATTTCTGTA CTTCGTACGGGAGGTCACGTCCTCGCCCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCCCTGTGTGACAGTGTGACCGCAGACTTGTCTACTATGAG/A/GJGGGGAGCTGTGTGCACTCATGCCCGCTCCCTGTGAGGCTGAGCCACTGAGAACTCAGCTGGAGTGGGAGCCACCTGGCTGGGGCCAGCCACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCCTCCCTTCCCTTACTCTCTGCCTGCAGGATGTGCG/A/GJCGTGTGCCTGGAGTAGCCCCGACTCTTGACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST4438 7	100 C --- 62 C T ---	---	GATAAGTACACTGAGGCCCCCAGGAGGTTATTGCCTAGTAGCCCCAAGTGTGCACTGACCGTTAACTCTGCACCAATGGCTCCAAAGCCCGTAGGGAACTGGGGGATCTAGGGGATGGTGAGGAATGGCCCCAGCCAGTCCCGGGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGGAGATGGGCTGGATGAG
ESTD-PBDA	103 A G ---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGGGACCTCAAGCTCGACTTCAAGGA/C/TJGTCTGTCCGACCTAAGCGAGCAGCCCTCAAGAGCCGAGCGAGTGGG
EST12839 3	122 A G ---	---	CCTTCTCATGCCCCAGATGGAATTCACAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGTCTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAA/A/GJCTCTACCGCAGCTTGCTCGCATACAGACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCCCTTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAAACACACAGCCTTACTCCAGAG/A/GJTCAGTCCAAGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTTATTCAACTGGATTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACATTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCCTTGGATTTACAGGGCACAAAGGCTCAGCTGAACCTGGCTA/GJCCAGGACCTGGCCCTGCACCTCCCTGTTTCTCTCTTCATCCCTGTCTTCTGCAAAAGCAATGCAGTGGCCAGCCTGCTGTGGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTGTGTGTGATGTGCATCTCCAGGCAAAAGCCAC
EST54419 8	88 A G ---	---	GATCAAGCAGTGCACACGGGTACAGATGGACCAAGCTCTCCACAGTGCACCATGAGATGGGCCATATACAGTACTACCTGCAGTACAAGGATCTGCC/C/JGTCTCCCTCGCTCGGGGGCCAAACCCCGGCTTCCA TGAGGCCATTGGGGAGCTGTGGCGCTCTCGGCTCTCCACTCTGAACATCTGCACAAAATCGGCCTGCCTTCTGCCTAAATTTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTTATGGCACAAATGATCACTATTTCTTGACCCCTACTTAC/A/GJATCCTGGGAGATGTTATTTGGGTTAGCGTGGTGTATGTTGTCTACTATAGTCCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAACTTGGATTGGAGATTCAATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCACTAGCCTAGTTCGTAGCCATTAATGGTTGTGCCTTAC ATTATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCGTGGAGGGCGCCCTAGCCGGGGCCCTGCTGGCGTGGGGTCTGGCCACC GTGGGAGGCAACCTGCTGTCATCGTGCCATCGCCCTGTTGGACTCCGAGACTCCAGACCATGACCAA CGTGTTCGTGACTTCGCTGGCCGCGAGCGACCTGGTGATGGGACTCCTGGTGGTGGCGCGGGGCCA CCTTGGCGC
WI-567b	48 A G ---	---	TCTACACTGACCCCTACCTTCATCCTCACCTCTGCTGCCTGGTTCGAGJAGCCCTCATCTCTTTTA CAGGGATCCGCCACAGCATCCCAACTGATCTGGCTTAGGTCTTCTCTCCAATCCATCTTCAAAAG GCTGCCACTGTGATCTCCCAAGGTGATCTGATGCTACCATCTTGCTTCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCCACATCCCTTTCTTGTTAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTATGTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCCACATCCCTTTCTTGTTAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTATGTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATATTACATTAGTCTCAATTCTGAAATATTAT TTTTTACAAGJTAGCCCTTTGATTATTTTGAATTCATTTGTACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAATGTCTAAATACATTTTGGGTCAACATCAAAATTAGAAAGAA CTTACAAAGTTTATTGCTTTATGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACCTCTGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA[C/T]TCTTAACCTGCTGCCCTTCAGTCAAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCCAGAGGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAGACTTTTACATTTTAGAC AGG[C/G]AGCAGAAGCAGCAAGGAGAAAGGAAGT

WI-2625	98 G A ---			---	GGG CAG T C T G G C T G T A G T G G T A G A C A G C A C T G A A G G A T G G A G A G A G A G A A A C A G G C A G A A G C A C T G T G G T A G T T A A C A A G G C T T A T T A G G A [G/A] C A A A T T G A T A C T C C C T G A G G A C T C G C A G A A A T T A C C A G C A G T G G A C A G G G T T A T C T G T G G T G A A T T C A G T T A T C C A C T T G C A G G A G A A A G C C A G C C A G C A A A G
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTTCTCTTA		GCCTAAGTGT AATCACAGGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]ACCCTGTGATT ACACTTAGGGCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GTGCCTTT	GGCTTGCTCA		CTTGTTGAGGG AAGGTCTTG	CCATTGTTGAGGTTGGTGGGTGCTGCTGTCATTCCCTCGCACTCAACAAAGTGGCTTGCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGCTTTTCCATGCTCCCGTGTCTTTTGAAAAATTCGACT TTATCCTGAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTTATGCCGC		TCAAGTATGC CTTGTTGG	CTTGCTACCATGCATTTACAGCATACAACCTCAGTGAAATGCCGTAACCCCAATTATAAAACAT CTTGCCATCGAAGGGTTATGCCGCGAGACGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAGATTTGGATGGATGAAAGCAGAGAAGGAGATGCTAAAAGTGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA GCCCTAGGGA		CCTGATGTCAC CAACATTTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATGGGAGATAGTTGGTAGAGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796b	29 A G ---			---	ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTGGCTCCCC
WI-1796	29 A G ---			---	AGTCGTCACTCTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGAAAGATGGGTGAGT AGTCACATTAAGGATTTTCCAAATAA[C/T]AAAATGCCCTCTGAAAAATATCTCTCCCATGTCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTCC		GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGACAATTCAGCTGCCGGATTTTAATAGATTTCTGCAGCACTGCAA CAGGAACCAAAATCAGTC[C/T]GGGTAACTGAGAGTGGTTTTACACCCAAA
WI-1959b	87 C T ---			---	GTTGTGCCCTGTAGCAGACACAGAAAGGCA[G/A]GAGAGAAAAAGCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ---			---	CTTGAGTATGCGTGGATTTGGTATACAGAAATGGAGAGCTGGAACATAATCCCCCATATACCA AGGGACAAATTTGATCTGTTTCTACAATTACAGTAGGAGACATTTATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTTAATTGAGTGAAATACCAATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCTTATAAATAGC
WI-1980b	140 C T ---			---	

WI-2015b	190 A G ---			TGTCAGATAGTCGGTCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCCAAGACTAT GTGTGAATCGTCTATTAGGGTTTGTCTATAAAGTCTACATGGTCTTTTCCAACTTATG/CATATACTT CTAATACCATAGAG
WI-754b	49 C T ---			GAAGGCACAGGGAGAGATGGCTGTCTATCTACCAGCCAGGGAGAGAAGC/C/TJACATTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTTACTTTAGA
WI-754	22 T C ---			GAAGGCACAGGGAGAGATGGC/CJGTCACTACCAGCCAGGGAGAGAAAGCCACATTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTTACTTTAGA
WIR-1b	56 A G ---			AGGCAATCAGACCTACAGAAGGAACCCCAATAAAACTCTGATGATCGTACATCC[A/G]TGCGCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56 A G ---			AGGCAATCAGACCTACAGAAGGAACCCCAATAAAACTCTGATGATCGTACATCC[A/G]TGCGCTG GAGGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
				TAATTTTAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGTGCTGAGATAAGA
WIR-3b	72 A G ---			TAATTTTAAATGGGGCCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA/TGTATCTAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGTGCTGAGATAAGA
WIR-3a	69 A T ---			GAGCCTTTCTAAATAAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-4	47 T ---			CGGGACAGAGACAGACAGAGAGAGTTCTGCAGCATTACACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGATCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5g	209 C ---			CGGGACAGAGACAGACAGAGAGAGTTCTGCAGCATTACACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGATCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C ---			CGGGACAGAGACAGACAGAGAGAGTTCTGCAGCATTACACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGATCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C ---			CGGGACAGAGACAGACAGAGAGAGTTCTGCAGCATTACACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGATCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTTAGG TTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCACTGTT AGGTTTGAAGGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-5a	37 A	G	---	---	TAACCCCTGAAACTTTGTCTCTCCTCATCTCAGGGGAGAACACAGACTTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTGGGGTGGGCGAG
WIR-6	63 A	C	---	---	TTCTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C	T	---	---	GGCGTCTATGACTATCCTGGTCAATGATTGACTAATGATTCTG[C/T]GCCCTTG
WIR-8	46 C	T	---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAAGTTGTCAGAAAGAGGTATGA[C/G]CTGAAG AAAGAAATTACTCTCTTTTGACCAATAAATACAAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WIR-2	56 C	G	---	---	TGTCTTGCTTATGCCTGCCTCTTCGCTTGGCAGGATGCTGTCATTAGTATTCACAAGAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCTGTTCTCACTC
WI-7069	93 G	A	---	---	GGTCATTTCTCTTTTATCTGTGAGGCAGCCAGCTGACTTATCTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	---	CACACTGTTACACACCTATATTTCAAGTTGGAAATGC[A/G]TATTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAATTAATGAAACATCCCT
WI-18612	37 A	G	TGC	CTTGC	TTGATTGCTG CTTGC

WI-18517	87	C T	CAGCCTGA	CAGGAATCAG	TGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCCCTCCATTGTGTAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCCTGAC/C/TGTTGCACTGTCCAAACACAACTGACTGC
WI-18668	76	C T	TAGGCAAAA	GGCGAAAAAC	GCTAAATTAAA CTGCACCTTTT GC	CGATTGACAAACCTTTATTTTCAACTTAGGTAAACAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA/C/TAGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	AGCATCTGGA	GCTGTCACTCT	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAA/T/C/GCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGGTCTCCGA	GGGTCTCCGA	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTTGTGAGCACCACACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC/C/CACAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29	A G	---	---	---	TGTGGCAAAACCTTGTATTAATTGCAAAAC/C/G/ACTTAATTTACAGCACATTCATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T C	GGGG	GTGTTGGGGT	GCAATACCAC TGAAGAGGAC A	ACCAGTCAATGTTTATTTGGAGGTTAAATCCTATTAGGATATGAAGGATTAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGTCTGGGGTGGGGGTGCAGAG/T/C/GTGTCTCTTC AGTGGTATTGCGGACC
WI-18533b	91	T C	---	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAAACCTCCCGAGATTTCCTTTATTT TATATTTTCAATTTTTCATCCTAA/T/C/TTACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G	---	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAACTCCCGAGATTTC/T/G/CTTTA TTTTATATTTCAATTTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A C	TTC	TCATCTGATAC CTTGTTCAGAT	AACCAGGATA AGGCTACAAC ATTT	GAGCATATGCTGCATGAGGACCCTTCTATCTTACATTAATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTTCAAGATTTC/C/AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A T	TCTGGGAAT	CCTGAAGGAA	ACTTTCAGGCC AGGGC	CAGGACTTGTGTGCTGAGCTGCAGACACAGAGCAGCTCATGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAAGGGGTCTTTCATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTA/T/GCCCTGGCCTGAAAGTGGCCCATCATTCATACCCCACTGTT CT
EST10030	98	T C	TCTCAAGTCCC	CATTTTGTTC	GCAGTGGTGGT ATGGATGA	TATTTATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT/T/C/TCATCCATACCACCCTGCTGATTG
EST10052	24	G A	GAGGCTG	GCTCACTTCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/G/A/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAACCTGGTGGAGTCAATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

EST10605 2	118 C G	---	CTCTCAAGTAG ATAAGAGGCA TTGTTT	---	CTTGGTAAATCACAGTTCTGTATTATACAAAAACITTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACITTAATTTGTGGAGATGCCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G	---	ATAAGAGGCA TTGTTT	AGAAAGAATT TTGTTT	CATGTGTAATCCCATGATTGAAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCT[T/G]AA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAAAACCAGAGAAGGAGCAC
EST11260 8	101 G T	---	---	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T	---	---	---	TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCACCAGTAGATTCTTTGGACGAAGAAATCCT TCTGTGGATTCAGCTTTACCGCCTTCCCTCATCTGCTGGTGT[C/T]TCCCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G	---	CCAACCTACTT TGGAGCCCT	TCCAGCTTTCT CTAAAAACTCC T	GAATTCGGGTATTAATAGCGGGTCCACAGGAGGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[AG]JAGGAGTTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGGAA
EST11772 6	74 A G	---	---	---	CCAGGAATAAAGAAAAAAGAGTCAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCCCTCA[AG]GACTATTTCTGACTATAAGTGAATAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A	---	---	---	CTTGCCATTATTTTGTGCATGTTGTTCTTAAAGGCTTGTAAGATAACTTGGAAATGTGGGAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAGTAGCCTTAAGAC
WI-16644	42 G A	---	CAATAAGCAG CTCATTTTGAT TAC	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCTCCACACAGAACTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G	---	TTGTATAATA ACACTCAGTA CAAAGTCTGT	GGCTGGTCACT TCCTGGAT	GCCTAGTAATTCAAAAAGGAACATGTTTGATAATAACACTCAGTACAAAAGTCTGT[AG]ATCCAGG AAGTGACCAGCCGACGTGTCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C	---	---	---	GTGGAAAAATTTTTTATCTGTTACGCTTTCC[T/C]ATTATATTTATCTTGCTCTGATTTTCAGCACCC CACCCGATTTGCAGGCAGTGTCTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTTCT
EST12492 1b	95 A G	---	---	---	CCCCTAGCAAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTTGCCAAAAATTAAGCTCTC TTCCCCAGAGGCCATTAACCTGAGATTAT[AG]GGAAACGCACAGCAAAAATTGACGATGCAGCTTTTTA CCTTTTTA
EST12492 4	25 A G	---	---	---	ATCTTGAGGTTTCTGGGCCCTGTCAG[AG]AAGTGACATCTTTTACTTACCACAGGTCAGGAACCCCTAT AAGAAACTGTGTAGAAAAAGATAICAGGTCAGACTTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATAACTAGGGAGAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAATGCTCAGGGGAAATGACCAATTTTAAGGGCCATGTG GTCGTCAGGCGATTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTGCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTCCCTGAGAT[C/G]ATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTCTCTCTCTCATTTATTCATTTGTTCAAAACACTGTCTAGTACCAACATTTGTCACCGGGC[A /G]TTGAGAATACAATATTGAAGAAGAGTCACTGCCCTGCCCTCTGGAATAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGGTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCTGGGAGTGACCGGATGGGAATCCATGTTGCTTTGCGTACCTCCATCAGGTCATTGGG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCCAAGTTATTTACCAGAAATTTTGTTCGGTTTCA ATGTAGTGTATTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAATACTGTTAAAAACAACAC[C/A]GTTCTGTCACTTG CAGAGACCCACAGGGACACACATTTCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAATGAAGCATAATAAACAGTTAAAAATCTCAGAAAAATCATCTATAGTTGA GTGTAACCTCCCTAAATCAGTCTTCTAGGGCCAC[C/T]GGAGCAGAAAGCAGCTTCCCACCCCAAG CACCTCTGAAC
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTAAAAATTTAATCGCTTTTATACAATTGACACCAAAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAAGCTGACACGTGTCCAACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTTAAAGATTCCTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTTCCCTCCACAAATATTTCTGTGTGCGAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCAATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATTT[G]GACTAACCAAGTTCTACAAATTTACATAICCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTACAACCAACTTGGCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACAGAGGGTT TGACAAAAGA	G	AAAGATATAAAAAACAACCTCCCATCAGTAGCAATACAAGGTTATACATTTTAACCAGATTTTCTCAGG CCTT[C]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCCTCTTGTATATAAACC

EST13278 2a	51	A G G	CTTCACCGAA CAATATTTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAAGACGTTTACAAGCTCCAAACCTTTCCACCGAACAAATATTTTAGG[A/G]ATTTGAAATTTAT TTCTGTAGTTCTCACCACCCCAAGAAATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAAATATTAGATAATACCTGTTGGGAAAAGTGTGCTGAATTACTAGCC TGCCTGAGAATCCCACACATTTTCAGTCCAAAG[A/T]AACCTTCCCTCAAAATTTTCCATCTCCCATCAGA GG
EST13290 9	39	A G CTT	CAATTTT TAGA AGTTTGGGTT	AAATCACATTCA TGGAAAATTCA G	AGCTCATCTGCAAGCAATTTT TAGAAGTTTGGGTTTCTT[A/G]CTGAAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGTGGGCTTTTTTG
EST13518 2	45	C G ---		---	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTGAGCAATTTA[C/G]ACTTTAAAAATTACCTCA ATGTTCTCGGAGTCGTCCATAGTTTAAATGACTTCGACCTTCTTATAACCTTGATTG
EST13522 8a	66	A G ---		---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTTGGCCCCCATCCCCGCGCAGTGTCTGGAGAC[A/ G]TTTTGATTGTCACAACTCGGAGAGGTGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69	T C ---		---	CTTTAAGGAAGTGAGCCAGATGAATCCAAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAGGAGGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101	C G ---		---	AAGATTACGGACCAATAAGAACTGCCCCCGACCCATACACACACAAATTTATAGCAGGTAACCA CTGAAAGGAACAAAGTAATGACTTCTTGAACAA[A/C]GTTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25	A G ---		---	CCTCAACCATCTGTAAACCGAGCCC[A/G]CAGTGACCGGGACTTGCTGCTTCCCCATCCAGGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23	A G ---		---	CAATGGTGTCCATGTGAACATAT[A/G]ACCTATTTCATAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAAATGACCGAACACAGGAGGTAGGAGG
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATTCTGTTGGCATGCTAGACAGAGGCATT[A/T]CTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCCCTTCACACTCATTTTAAATTGT
EST14812 2	50	A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGAGTTTGCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128	A T	ICATACCCACC ATACTGGTT	CGGGAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCCGCTCTCCCCACTGAACCAAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAACTTGCCCGTCAACCCACCATACTGGTT[A/T]TTCC GGTACTGTTTCCCGTA

EST15420 6	109 C A ---	---	---	TTTAAACCCCAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTCTGCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTGATCATATAATCATATAGCCAAAGGGACTC/AJGGAAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	---	---	GTCACACAGCCTTTTATTAAGACGTGAAAAAGACAAAGACAAACAGAGGA[G/C]JAGCAGAGAATAATA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	---	---	AAGGATTGAAAAACATACCTAGATCATATAAAATTTGTGAAGGTTTTGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATTCCTCCAAGGT
WI-16782	96 C T CACTGTAAGG	---	---	CTTCTCCTCCTAGACGTGGAATACACACGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAGGA[C/T]GATGGAGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTTGTGGG
WI-16783	64 A G G	---	---	AAAAATGTAAACCTTAGAGTTGCCCTCTTTTGTGTACCTTTTCTGAGATGCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---	---	---	CAGGACTTAAGGTCAATTTGCCCTGGAAGACTTTAACTAAAGTCAGGGCAACATAGGA[T/C]TGTGA CAGCACCACCTGGACCAAGAGTCTGAAAATCGTCACACTAGCTGCCAGCCCTTTTTCCTGGC TGCTCTGCTCCAGAGC
EST16088 8	89 G C ---	---	---	GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGACGC TTTTCCAGAAAGGCCGCTC[G/C]GGGTTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---	---	---	CGTCTGAAGTTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAAAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[T/J]AAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---	---	---	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTTGTTTCACTCGTCCATGCTGTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---	---	---	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCCAGGGNA/GJTTGGCCCCGAAGCTGGCTCAGTCACTCCAGGACCTCAGTC
EST16118 0b	119 T C ---	---	---	ATGGTATAACAAAATCAGTCCAGGTTTTTTTCTGAACAAATGATCCTTTTGGTCTTTCCCGTGGCATG CTCTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---	---	---	ATGGTATAACAAAATCAGTCCAGGTTTTTTTCTGAACAAATGATCCTTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAAACCCCTACGTCTAATCAGTCACCTAAGATAATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGAGATT[C/T]AATGAACGT AAATAATTCAGGCAATTTTGATCTAAAGCAATTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGATAGGA
EST16182 6	54 G A ---			CATTGGTGGGTAGGGAAGATAGTAGTGCAAAATAAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATGAAATTTATTTACTGAGGGTGATAGCAGAAAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAACCTGTGGTTCACAACGATTGTTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTCTCTCTGCCCCCTCTCTCGTTTCATATTTTATGTCACGTCTCCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAATCA[G/A]ACAGACAGATAAGAGCTTTTAAGTATTTTCGCATTT CCCCAGAGGAATAAGTCAGCATCAATAACCATGGGTACATGCTCACGCACATGGTGTCTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCTCAAGTCTGAGTCACAGTTTCATTTGGGAGT[C/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATCTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCTCAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATCTCCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCTCACACCTCATTGGCTGGAACCTGGTGCACATGCACATCCCTTGAACATATCATTTGGCAA AGGGAATGGGTCAATAAATGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCCTGTGGCTTGCTCTGCTCCAGCTGCTGCCAGTGCCACAG[G/A]TGGTCTAGCCTCATGG CAGAAAGCATTTAGCCCACTCTGCTGCTGCTCCACTCTCTCTCTCCGCCGCTGGGGCTCACCACC TCTTCCCTCCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGCGAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGCTG	TTCTTCATAAG	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGCGAGCTGTT[C/G]TTCCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---	CAATAAGCA		TTGCTTTTATTATCCAGAAGGCATGCTACAGATACTGTACAGCATGAACATTTATTCATTACAAA AATGGCTTCCAAACCATTTAAATGAACCTT[C/G]GGAATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	GCTAATGGCA	TGTGAATTGGG	TATAATCCATCTCCAACACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAATGTTTCTTGATTAAGTGGAGAAATCTGCTCTTTATGTA

VI-16879	79 C T	GATACAGGC ATAATTTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAACAACCTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCACCCAG
VI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAAATTTCTCCCTTTACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGCTCTCTGAC/A/G/GCGAATTTACCTGACATGTGTCATCTCCCT
VI-16888	70 G A	GCTAATTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGAGAGCAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
VI-16905	75 C T	ACTTGGCCTGT GTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTTGTTTGTTATTTGCCCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACTTTGGCCTGTG TTGTTCA/C/TJCCCACTGCCTAGAAAGATATAGACA
VI-16910	74 G A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAAGATAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACCTTATTTGGCCTGAACCACTGAAGGT
VI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAGAAAAATAAACTACCACCATTTCTCTGCTACCACAGAGCACTAAAATCTAGGAAATTTGAC TTTACTGCAGCCATTAAACACGAC[C/T]GATGCCACTTCTGTATCAGGAACTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
VI-3947b	127 A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGG[A/C]CCA CGGCAATCACATGAGATG
VI-3947a	58 C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGGACCA CGGCAATCACATGAGATG
VI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTGTTTTACTTTAAATGCACACTACATAACAACCTAATA[T/C]CTTAACTTTGGTCCAACATTTT AGTATAACTAATAGTTTTTACTGATAACTTGCAATGCCATTAAA
VI-16995	55 T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATT[C]ACGGCTGG AAATCAACATGCCTCTCTCTGTGAAGTTGTGAGCATGGAGCTGAGAAGGCTGAGTCAATCT
VI-3992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTGCGCCTCATCTGAGAT[T/G]GTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA
VI-3992a	46 G A	AAGCACCAG AAGTACACTG	CACATTCCCTT ACAGTCCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTG[C/G]CCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA

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VI-17010	23 T C	TTCAACAGGA	AATAATACGGT	ATGTTTCAACAGGAAAGCCATGTCATGACATTCAAAACACCGTATTATTAGAAAGCTCATTTAAT
SI-17127		AAAGCCATG	GTTTGAATGT	TGTTTAATGCAGACAAAAATCAAGGCTAACTAAAGCAGATCCAAATGACCCAGTGATCAACCTAGA
b	74 C T	CACTCGGCAC	GGGAGGGCAGG	GGTCCACG
		AGACAGAGT	GGTG	ATCCGTCTCCAAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA
VI-17040	94 T C A	AAITCTCTTAT	GGACTATGGCT	CAGAGTTCCTGGGAGCCATGGGCACCCCTGCCCTCCCCAGGCTTCTTAAGTAACAACT
		CATCTCAAGCC	TATTCAGTGAT	CACGCGTTCAATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
			G	GAGAAATCTCTTATCATCTCAAGCCAGTTCATCACTGAATAAGCCATAGTCCAGTCTCGTTTTCC
				AAATCTTCTCATATTGT
II-17044	47 G T G	GCCAAGGGAT	GGGGATCCCC	TTGTTTTGTTTTTTCTCTCTCTGCCAAGGGATTAAAGTATAGGTCCTTTAAACAAGGGGATC
		TAACGTATAG	TGTTTAAGA	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCCTGCAGAAATGGCAGGAAATCGAAT
				CAAAAGAAAAGCAAGTG
II-17021	62 T A ACTC	TGGACTTGTC	TGTAGAGTTAG	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCCCTATAACTACTCTTAJG
			TGGCAGCTGC	CAGCTGCCACTAACTCTACAGGCACAGTAACACTTATACAGGAGCACATGCCAAAGTGCCTGG
				GAGGTGCCAATAAAATCAA
II-17065	90 T C CTT	CCAGAAAGGA	CCCAAGAGAC	TGTAAAAATGTAGACATGGGGGAAAAACATTCGTAATCAACATGTGCTGTTTTCTACTTCCGGTA
			AATGAAATCCT	CCAGAAAGGAAAAGCATAAACTTTCIAGGATTTCAATGTCTCTGGGT
II-17066	32 A C T	TGTACAGCCA	GAGATGTTGAA	TTCATAAGGTTGTACAGGCCAACATCACTGTTTCATTCAGAACATTTTCAACATCTCAAAAAGA
		ACATCACTGTT	AATGTTCTGGA	AACCTGCACCCATTAGCAGTCATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
			A	
II-17074	86 T G ---		---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT
I-17104b	108 T C ---		---	AACCTCCTACACAGGCCITTCATACATAGGAGTATATTTGGCCAAAGACTCACCACACTAGAAGTGATT
				CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCCGTGATGCTTGGAGCTTTCCCATTCATTCCA
				AATCAGAAAGCAGTCAGTGGCCCCGTGGTTCCAGACGGCTTCCTCTCTTTGTTAAGAAATTA
II-17114a	37 T C	TTCCATCAAG	TTGTATTATA	AGGTTCCAAACAGATGTTCCATCAAGGACTTTGTTTTTCCTCTCTCACTGCTGCTATTATAATAC
		GACITTTGTTT	ATAGCAGAGTG	AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAGAAGAGACTGCAGCCACAATCAGAGTTACAT
			AAGAGAC	GGGA
		GATGAAATTC	TTCTCAGAATC	
II-17150	76 T G C T C T T	AGATAGTCTTC	CTGGAAGATAT	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAAATTCAGATAGTC
			G	TTCTCTTTTCATATCTCCAGGATCTGAGAAGGGCCCTCTTTGCTGCTCTAATTT
		CATTTCTTTGT		GAAATCGAATACGTCCATTTCTTTGTAAAAATAACAAATAACGTTTCAGGCAAAAAGCAAGATTCTG
I-17163	43 A G TAACGTT	AAAATAACAA	CAGAATCTTGC	TAAACCAACATTGGAAAAGGGGACACAGGGAGGGGCAGAGGGGAAAGGGCCAGATTTTCAACGGTTT
			TTTGGCCTT	CCTCCACATCTGCAGACAAA

VI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCTCCCAATTCATTAGCTATGAGGATTATCAGTTTCATTTTCAGAGCGAATTACTGG
		CGAGGAGC	CAACTGCTTC	GGCGAGGGGGTTTAATATCTCTGATGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGC[T/C]AGAA
NI-7180b	81 C G	---	---	GCAGTTGAAAATTGAGGG
NI-17180a	47 T C	CACAAAAATA	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCTGCAC[T/C]CCCAAGTCTCGTCGCACAG
		TAGAGAAATCC	TGCGACGAGAC	GCTTCAACAAATTAC[C/G]AACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
		TGCA	TGCG	GGAGTC
NI-17156	54 G C	TGTTCTCTAAA	CAAGAAATAT	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAATCTGCAC[T/C]CCCAAGTCTCGTCGCA
		CTTTAGATATC	ATATTTGATTTC	CAGGCTTCAACAATTACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAG
		TCCCA	TGTGGAA	GGAGTC
NI-17149b	79 T C	---	---	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAACTTTAGATATCTCCCAT[G/C]TTCCACAGA
NI-17149a	48 C G	CAAGTTTGA	CCACGCACGTG	ATCAAAATATATTTCTTGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT
		AGGAGGAACA	CATGA	TAATATTCTTG
		---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGACGTGCGTGGAA
NI-17197	67 G A	CTGGGGCTAC	GCATACC	ACCCAAATTGTCAT[C/G]GTGATGAACACAAAAGGATGGGAAAGAACACATTTCTCTACA
		---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACAT[C/G]TCATGCACGTGCGTG
NI-17198	38 A C	CCTAGTTT	ACTGAGAAATT	GAAACCCAATTGTCATGTGATGAACACAAAGGATGGGAAAGAACACATTTCTCTACA
ST18753	27 C T	GGTCTCAT	GCCTGA	ATTTTGCTATGTTGCCTGGGCTGGACTCCAGCAATCCTCTGCCTCAGCAGAAGTAGCTGGGCTAC[G
		---	---	/A]GGTATGCACCACCTCACCTGCTTATCAGTTTCGTTTAAAGAAATATTGACTTTTAGATGCGCA
VI-7108b	74 C T	CA	CC	TGTAATTCAGTACTTTCTCCCTGCTGCTAGTTT[C/G]TAAATTTCTCAGTGGACAAATGGACAA
ST19067	41 A G	---	---	ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
		---	---	TTC
VI-7108b	74 C T	CA	CC	TCGCTATGCTACCCAGGCTGGTCTCAT[C/T]TCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG
ST19067	41 A G	---	---	GATAAGACACAACTGCCACCGCCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
		---	---	TTATTTAAACATAACCAGATGCACCTGGTTTTTACATTCTCTGGTTGCCATTTCAGTCTCAAAGT
ST19067	40 A C	TTT	CCA	AAACAC[C/T]GGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACATTACAGAGT
ST19125	28 A G	---	---	ACACAAAAATTACCATCGTGACCATTTAAGGGTATAGTTCA[A/G]GTGGCATTAAAGTACATTCAACT
		---	---	TTTGGCAACCCGCCCATCACCATTTCATCATCCATCTCCGTT
ST19067	40 A C	TTT	CCA	ACACAAAAATTACCATCGTGACCATTTAAGGGTATAGTTCA[A/G]GTGGCATTAAAGTACATTCAACT
ST19125	28 A G	---	---	TTTGGCAACCCGCCCATCACCATTTCATCATCCATCTCCGTT
		---	---	ACACAAAAATTACCATCGTGACCATTTAAGGGTATAGTTCA[A/G]GTGGCATTAAAGTACATTCAACT
ST19125	28 A G	---	---	TTTGGCAACCCGCCCATCACCATTTCATCATCCATCTCCGTT
		---	---	CTGTTTCTCAGAGATGACACTGCCAACA[A/G]TCACAGATTTGCATACAATACAGTTATGTATTGGC
		---	---	TATTCACAAATTTACAGTAGTGTGTTTTCTCTGAAAAA

EST20824 3	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACCTCAGGGATTGAGGTTTTTA AGGATAACCTTGGTGAGTAGAGGGCCAGTAAGTCGGAGTGCTGATTGTTGTCGGGTCCAAGATAAAA ATCTTAGG
NI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTTACGAGTGGGACAAAGTGG ATGCTTGAAGAACTCAGTCTTGAACCTCAGACAGCAATGGAGCGGGATGTGAGTGGGACCA
EST21904 2	128 G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTTTC AGAAAGCAT	TGATTGTGGGCTGGGAGCAGGTGGGCAGTTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTTCTGAACACCTGOC
EST22111 3	82 T C	GAAGATCTGT CTGGCATTCCT	TGGA AAAACA GCCCCAC	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGTCTGGCATTCCTTTTTCJGTGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCTGCTCCATTCJACCGCATCCTTCATGGTAGAGTATCAAAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAATCCACCACCTGTAAACAG TAGCATTCAAATGGTTTTTACTCTATTCJGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAATCCJAGJCCACTGTAAA CAGTAGCATTCAAATGGTTTTTACTCTATTCJCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATTCJACATAAAAATCCACCACCTGTAAA CAGTAGCATTCAAATGGTTTTTACTCTATTCJCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C	---	---	TCGAGGAGCTCTGAGGAGCJACJACCAAGGGAGCTGTGTCCAGGGCCACCCTGCAGGCAAGTGTG GTCCAACCTCCCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTTAACTGT
EST22433 2	103 A G	AAGACATGTT CACCAAGTGA GAA	CAGCTTCAGCT TAAC TGACAGA	GATGTTAATGACTTCTCTTGAGATATGATGGA AAAATATTCAGGTACACATGGAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACCJAGJCTGTGAGTTAAGCTGAAGCTGAAATTT CTGGGAGCTTGACATGCTG
EST22657 2	71 A G	AAATGGATCC TTATCTGCACA	GCATGAATTT T	TATCCATTTCAAGAAAAAAAATGACTTAAAAAATACAATTTCTATCCAGAAATGGATCCTTATCTG CACAAGJCCATTGAAGAAAAAAAATTCATGCAAACTGAAAACCTATGCTTT

ST22993	71	T C	ATCCTTTTGTT TCTACCCCC	TTGCGTGTTAA TTTGACTGTAA TG	GCCTTTTATTGTCTCCTTTTAAACATCAAAATGTTTATAACACACTTGATCCTTTTGTCTTCTACCCCCA ATT/C/CATTACAGTCAAAATTAACAGGCAATATAATAGGTCTAACAGAAATGCTTGCAATTT
ST23021	108	T A	---	---	TTATTTCTCAGCTTACCAATTTGTGACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAAATCTTTGCCCTTT/AJATGGTTTTGACAGTTTGTGTCTTTCT T
MI-17387	55	C G	CCTTGCAGAT TGAAGAAAA	GCTTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTTAAACATGCAAGTTTCATTTACATTAACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG
ST23669	101	A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCTCC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAAGAGAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAGCTCCAGAGGCAG[A/C]GCTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGGCTGCTCACTG
ST23733	31	T G	GGCTGTTAGTT TTGTTTTGTTT	TGCACCTTAA TCCCATCAAT	AAAGGCTGTTAGTTTTGTTTTGTTTTTCCCTTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCCAAGGCTAGAGAAAGATATAGGCCCGAGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
VI-17470	83	A G	GTCGGTCCCG CCAG	CCAGTGACGAG GCCGA	CTGACACGTCCCTGTGTGGGGGTGTCCTATGTGGCGTGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCT[A/G]TCGGCCTCGTCACTGGCCTTGTCACCTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCCTCC
VI-17519	55	T C	GTTGCTCAGC TAATGAATGC	AAATTATTATTT TGACGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTTGTCTAGCTAATGAATGCA[T/C]JAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAAAGCTTAGAACAGTACATGGTGCATAG
ST25356	95	C G	---	---	TCTTGATACAGGTAACCAAGTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTCTTTTT
ST25356	26	A C	---	---	TCTTGATACAGGTAACCAAGTTTGT[A/C]JACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTCTTTTT
VI-7581c	99	C T	---	---	GGGTGACGCTCCAGAATGGAGACAAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCACACATT ACTACCAGTTATTTGATAATGATAGAACCCAA[C/T]TAGCGCAATTTACATTGACGCGTCATGC
VI-7581b	86	T C	ATTGATAA ATTGCGCT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAATGGAGACAAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCACACATT ACTACCAGTTATTTGATAA[T/C]GATAGAACCCAACTAGCGCAATTTACATTGACGCGTCATGC
VI-17596	86	A G	ACITCCCTGTG TAAACACTCC	CATTCCTTAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAGGCGCTACT TCCITGTGTAACACTCCC[A/G]ATATTGTCGATTTCAGCTATAAGAAATGGGCCACTAAGTGGGTC

NI-17623	46 T C ---	---	TGTGGTTTAAATTTCCCATATAATTAATGGTGGGCACATTT/CJGCAATGTGCTTACTGGGTC ATTCATATACTTTTGTGAAGCATCTGCTCCAACTTTTGGCTGACATTTGGAGTTTTTTGGT
EST26419 1b	46 T C ---	---	ATTTACATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGA/T/CJGGCAGTCCAAAACCTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGAGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	CAAGAAAGTTTG GACTGCCOC	ATTTACATACAGAGATACAAAGGCAACTATGTGCAG/C/AJACAATCTGATGGCAGTCCAAAACCTTCT TGGGAGGAAGTAAATTCATGGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGAGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C ---	---	TCAGCTTTAATTTAAGGACATGTAATAAAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/CJ/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTCTGCTGTTCCATCTTGGCTTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---	---	TACITCAGTTTAAGGCAAAATTCACACAGAGACTGTCTC/JAGJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGTCATGACGGGAAGCAGAG
EST27152 1	101 C T ---	---	CAAAGGATTTAATTTGTTCCCTAAAAGTAAATCTAGAAAAATAGCAACCCACTGCAAGAAGAGTT CTATACTAAACATTTTCAATCATCTCTCTCTC/JTTCACATGGTGTACTCTTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 2a	33 G A ATTT	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACITTTGCAACAATTTAATAATTTATC/GAJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTTCAGTATTCTGTACACATTTCTGTTAACAAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTTG C	TTATGGAAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAAGGCCAGTCACATCTGTCTCCAGTCTTG/C/JJAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAAACACACACTCTTGTITAGGAATGTTT
EST27788 3	100 A G ---	---	ATTTTATTAGGCGGTACAATTCCAAGGTGGTAAGGGTGAAAGGAAAGGCGAAGGCGAGGCAAAATACAT TATTGAGCTGAATAACAACCTTTACATTCAAGGAC/JAGJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGIGGAT
EST27828 1	58 G A AGAACCCAC C	GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAAACITTTCTTCTGTGGATCCCAAGTACGTGGAAGTCATCAGAACCCAC/JAJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAAATTTTACTTGAA
NI-18369	58 G A ACAATC	TCAAGAAGGCC TTATCCATTT	TAAAAATTTGAGATACATTCGCCCAATGTAACAATAAATTTCAATCTGTACACACAATC/GAJAAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAAACGATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---	---	TCCCGCTTCCAAAAGCTTTATTGGCAAAATATGCTCTAT/JAJAAAGAATGATCAATCCTGTTGCCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACCGCCGTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTCGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTTAAAT/ATAGGTATAAAAATAAAATGCGAGAAACATTAAAC GGAGAATGTACAGACAACAGACAGACATGAGTTTGTCTGACTGTGACACATTTGGTGAAA AGAAATGGTCTAGTAATCGTTACAGGATTCGGGTGATGGCCCTCCCTGTCT/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGATTAGA TGAGCCTGGGGAGAAAGACACAGAGAGTGAAGTGCTATTAGTTACATACCAAGGTGACATACTG TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGTGTGCA
WI- 17730b	68 T C	---	---	
WI- 17730a	39 A C A T T	GACCACAGAA GTGAAGTGCT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACACAGAAAGTGAAGTGCTATT/CJGTTACATACCAAGGTGACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGATGTGTGCA
EST29041 5b	53 G A C A	GGAACAAACA CATTAAAGCAT	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCATTGTCACT[G/A]GCTAACTCCT CAAATCAACAATACCTTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTAGAAAGGACACCAGCTCTGTTGGACTTAGGGCTACCCCTATTCACGAGGTGCC[G/A]GTTATTT TCACCTGGTTACGCTGTAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGGACACT
EST29912 3	103 C T A C A G G C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGTACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCTC/TACAGAAGAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 3	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAAGTTAACTCACCATGAAA TTTAACTTCTGTACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	99 A G	---	---	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATTCTTTGAGTTACAAGCAA TCCAAATTACACTCTAAGTTATTTTAATATTC[G/A]GGATTAAATTTCTTCTAGTTCAATCTTGGGA GG
WI- 16260b	86 G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCCAGA GTTTCACAATATAGGTAGC[G/A]ATAACCCAGGCTCACTTTCCCTCCGTGAGAACTTCGTGGGAC
WI- 16260a	59 G T A	TGAGGTGGATT CAAGAAGAAA	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAA[G/T]ACCC AGAGTTTCACAATATAGGTAGCAGTAAACCCAGGCTCACTTTCCCTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A T G	ACAGGAAATA TTGTGCTTTCT	TGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATAATTGTGCTTTCTT[G/A]GCCTGTTTCCCTATACCCCAATATCATAAGAAAT GTTGTGCTTCTATAATGTTACGCTTCAAATCTTTTGCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTTCAAAA

EST31951 4	87 C T	GGGTGTCAG CCAACA	CCACCAAAT CACCTOC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCAGCCAAACA[C/T]GGAGGTGATTTGGTGGGAATTCATTATCACAATATTCT
EST31968 8b	95 T G ---		---	CGAATTTGTCTCTCTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT[G/A]ACTGCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTOOC
EST31968 8a	75 T C T	GCGGGTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCTCTCTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTTT[C/A]ATAATGGGATTTTCTGCTTAAGTCCCACTGATTCTTACATGGGAAAGGTGCAAAG ACAGTGGTACTGCTOOC
EST32063 2	103 C T ---		---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTCCAGGCCCATTTGAAATAGCAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G ---		---	AAGGCTTTCCAAAGCATTCAAAGGCACTTGGGTGTTGTCCTAAGTTTCTGGTCACTGCAGCCCC[A/G] TTCTGTATTAGGGAGCACCCCAAGCCCAAGTAACAATATGGTTCTTGCG
WI-17800	29 C G	GGGAGCACAA GAGAAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAAACTCAC[T/C]G/AAGACTGGGATTAATTGTAGGAATATTTACACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34 T G C	CCTAAAGCTCG GGATGACTTTC	TGGCTTAGGT TCTACTTGATG T	AAACTGTCAITTCCTAAAGCTGGGATGACTTTCC[T/G]ATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAATCAGAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAGCTGAATTAATGTTCAITCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAACAAAATCTTTA TAGTGTCCAAAGATAAATTAATCTTGTTTAAATCTTTGCCAGCAAAGCAAATA[T/A]CCGCACTGAC TGCTOCTTAGTCTGTGATC
WI-17860	121 T A	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTGTTTTATAGCCTACTTCTCAAAATTTGTT[A/T]TTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACTACCA
EST33301 4c	43 A T	TTTTATAGCCT ACTTCTCAA	CCGTTGTCACT AATCACACAA A	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCATGATC AATGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	80 G A ---		---	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	63 G A ---		---	
		AGCGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATTT	CTATCCAAAAGATATTTATTCAGCGGTGTTTTCAATACTAAACA[G/A]TTGTAACAATGCAATATT TAACAATAATACAGTGATTAAATAAGCCATGGCATAATCCAGTTGATGTAATACTTTTGCAA
	44 G A CA		GCAATGTT	

WI-17904	50	A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAATGAACAC[AG]TACGGGAATTAC TATTAAACATAAGCGGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACAAACACAAATGA GTTTTTCTTTGAGTGACACAAGCTTGTTCAITTTTGGAGAAAATGTGTGCCAAATACTCAAGTGTGAA T[AG]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34149 5	69	A G	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAACATA ATAAAATC	TGGGAAAACATAAGTTAACTCAAGAATATAATCCAGTCTTTATGTTACTAAAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C]A[AT]ACAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
EST34343 8	95	C A	---	---	GGTACACAATTTTAAATGGAAGGAACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCCTAAAAAGC[C]TGGGAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAGTTTTTCAATCA
WI-17982	98	C T	CCTAAAAGC	CCTTCC	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTTATGATAAAAAACCTCTCATTTGTGA AAAAACAGCTAAGGGTGACATCTCCAGACCCCAACCACTGTCCCTGTAATGTT[AC]TGTCTGAGAGTCC ACATTTTGGAATCCAAT
WI-17993	118	A C	---	---	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAAACAACATCTCCCAGGCCTCGCAGT AGAGCGGAAGGGAACAG[AG]GCTGCCCATGTGCTCTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33	C G	---	---	ATTCTTTATAAAAACACCATGTCCCTAAAATGT[C]G[AT]TCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24	A C	---	---	GCCACTGAAAAAAGGTGCTCTCC[AC]GTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAATACTTAATCA
EST35164 8a	57	A G	CACAGCCTGC OCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCC[AG]TCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTAGGTCCTCTGTGACATTTCCCTCTTG
WI-18052b	67	A G	---	---	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTTCATGTACGAATC[T]CTGGTTACACATCTT[AG] A[AG]ACAGCAGAGCTGCTGAGGGAGGGTTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGCTGGC ATGGCCCCATCCATGCTTT
WI-18052a	50	T C	CCTGAGTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAATGCTACATAGGCTCCCTGAGTTCTTTTCATGTACGAATC[T]CTGGTTACACATCTT AGAACAGCAGAGCTGCTGAGGGAGGGTTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGCTGGC ATGGCCCCATCCATGCTTT
WI-18054	46	A G	GGGAGTGGG GAGTAAAA	CGTCACCTGCG TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAA[GA]TGGAAAGCAGGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A A G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGTGCCAAATCATCTCTCAAAACCCTGTGGTAGCTGCTAAGCTGTATTTTCAGA[G/A]GAATGTTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGTCTATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCAATTCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTTGTGTCTGGGCTTCAT GGGATGCATAAAATTTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGTCTGGATCAGAAAAAAAAGG CAGGCA
WI-18070	28	A C G T G T A T	AACCCACTAC TTACTCAGAGT	AAAACTAATA AGAAACTGGA	AAACCCACTACTTACTCAGAGTGTGTAT[C/J]ATATTAAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATTTCTGTACTCAGAAAGCATTTTAGTTGCAAAAGGATATAA
WI-18080c	80	C T ---		---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTTGTAAATTAATCTACTATGCCGTG TTTGACTTTTAT[C/J]TCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65	G A ---		---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTTGTAAATTAATCTACTATGCC[G/ A]TGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41	T C A G T C T C T	GCAAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCT[C/J]TGTAAATTAATCTACTATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18086	63	G A ---		---	GTGGGCATCCTATAAAAGCAGCCATGTGTGAACAAATGATATGCACAGAAAGCATCTTCT[G/A] TGGCTTTGTACACGGTTTCTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71	C T ---		---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTACCTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70	C T T T	TTAGTGTACCT TTGGTATCCC	AGAGGCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTACCTTTGGTATCCC TTC[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78	A G ---		---	TTTGTAGAAGCACTCTGTAAGGCAAGGATGCATTCAAAAAATGGCTTTGAGGATTAACTTCTCTTTA GGTAAATTTGC[G/J]TAAGAACATAAAAGCATTTTAAAGTCCACTGCCCTTAGAAACT
WI-18169	115	A G G A G C T C	CCATCTTCCG	GAGTCTGCTT GTGCTCCA	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTCCACTATGAAGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGCT[C/G]JTGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26	G A ---		---	TGAAAGAAAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAACAAAGGATGAAGCTAATCATGAG GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62	G A	---	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT TTG	---	TGAAAGAAGTCGACACAGCGGACACTGTGCATAAAGTGGAAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGAAATGAGCTGGAGACATTAATCCTGGCGA GACAGTGAAAAACATTGAAAAACACAAAATACAAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGIGTGAAAAATATATACAACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGIGTTCTTGAAC ATTACATACAAGCATTTCTGAGTACAAACTAGGGACAGGTATTTACAAAAACAATAAGAGCAGA GTTCTGCCCTC[A/G]GTGTGCGGGGGAGAGAGGGAGGATTTCAGCATTTGGTGAGTATGTTAATT CCCTCAAGTTAATCCCTC
WI-18181	100	A C	CAGATC	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT OCCCC	---	CAATTCGAAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAAAACCTTTATTTTGAATTTGAAGTTTGTCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-18215	78	G A	CTGCCCTC	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT C	---	TTTAAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAAAACTTGAGTTTGAG ATCACATAT[C]CTGTCTCACTAGTCTATTCACCTCTGIGGGCATTCGGCAGAAAGTGGC AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGAGGTCAGAATGTTTCTTGCCTATATC TGCAAAAGATCGAACAAAG
WI-17892	76	T C	ACA	GGAAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA GCTAACACTTC	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18242	30	G A	AATCGTAACA	CCCCAAATGTT AATCGTAACA	TACTGTAAACAG CTTTC	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266c	119	C T	---	---	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124	T C	---	AAATAGGAAA TATGGACTATC	TTTCATGCATCA TTTGTGCA	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97	C T	TTCAAA	---	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73	A G	AA	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAAG	---	CTGAGCCTCTGGATATGTGTTAGTGTCTATCATTAATTTTGGAAAGCTGTCAGCTATTGTTATTTT AAAT[A/G]TATCTCTGCTCCCTTTTCTCCCTTTTCTGGGATTCTCATTTCTGCATGTGTTATA
WI-18330b	66	A/G	---	---	---	---	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGATAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAAATAAAGAACATAATTTTTTGTGAT TCACA

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WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGCGAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACAATAATTTTTTTTGTGAT TCACA
EST37564 5	85	T C A G A	AAATTCAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAATACTGCATGTTATTTAAGCTAAAAATTC AAGCCATCTACAAAAGATT[C/T]CTCATTTAGGGCTCCATAGGCTGCAAAACACATCAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---	---	---	GTGGCAAGAGCAGCTAAACACACTCAATTTGCATGAACCTCCAAATACGAACAGTGCAAGCTGATGG CCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACG[G/A]TTCAATCTACATGGCTGCTTTCGCTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---	---	---	GTGGCAAGAGCAGCTAAACACACTCAATTTGCATGAACCTCCAAATACGAACAGTGCA[C/T]GCTGA TGGCTGCAGTCTCTGCCGTGCTGGCTCTCTGGACGTTTCAATCTACATGGCTGCTTTCGCTCC TCTGACCTCCCCATTCC
WI-18357	89	C G G C A T C A A	CCAGCCCTTA GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTTACCGTGTGAGGTGCCATGAAGCCAAAGCCCATGGAGAGACATTTCAGA TAATCCCAGCCCTTAGCATCAA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A G ---	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCCTTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTT[C/G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCCTTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTT[C/G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTGC CCCTT	TCAGCGTGAT CAGGAAACA	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCCTTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTT[C/G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---	---	---	TTTTATCTGGTCAAGTCTCTTCTTAATGGCCTGAAGGTCACTCTCCTTTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTT[C/G/A]TGAAGTGTTCCTGATACA GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCAATTGTTAGTAAGTTTATTAAATCAGCTGACTTAGCATTTAGCATTTGGGAGATTATCTGGAT

:ST38512	91 T G	TGACGATGCC	CACGTGCACTCT	TAATAAAAAC TGACCCCAATTGGTAAACTGTGCTGGACTGAGAGAAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAATACTTCGT/G/GGCTCCAGAGTGCGAGTAACTGTTATAGCC
:ST38519	24 C T T	CCTGCACCTCC TAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACCTCC TAAAGATCTTTTTC/T/CCCCCAAGTCTTAACAGAAATGGTATATCTCTCTGGAAAA AGATGAACGTCATCAATGGAATTGTGCTGCTCTCGTTTTCAGCTTTGATTTTTTGTCCTTGAGAACCTTG TCCTCCCTGCTGATT
:ST38575	66 T C A A	GAACATCCCA TGTTCTGTGTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAAAATGTAAAACTAATGGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/C/CTCTTATGTTATACACTACCTCCCTTCTCTTCTTATACACATAGATTTTCCCTTAATTGCAGC CCA
:ST38616	101 C G C T T C	CCTGCTCGGC	GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTCAGCCCCGGGCCCCGTGG AGTC TCCGCGGGCCCGCCCTGCTCGCCCTTC/G/GGCCACCATCCATTCTCTCCAGGGG
:ST38652	59 T C C A T T T C A A	TCTGAACGTGGG	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTCTCTGCTGCGAGCAGGAATTAATTCAGTCTGAAC TGGGCATTTCAA/T/CJCGGTG GTATTTTTTCTCTTCATTTTGCAAGTAAAAAATCAT
:ST38654	42 T C G T T T A C A	AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAAATGGTCATTTTAATATATCAGTTTACATA/T/CJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTTGGCCCCAGGAGTTGGTTCCAGCATATA GGATCCTCACTCACTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCC/J/GJAGGCCAGCGGGATGTGTGCCCTCCTCTCCCACTCATCTTCAGGAACACGAGG ATTCTTGCTTCTGGAAA
:ST38759	86 A G G G T A T A T G G	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGTTATCTTCACTAGAGGGGAGAAGAAATCACTACCTACCTTTTGGATGCTCCCTCACTCTACTTGT CTCCCTGAGGTGATAGG/J/GJCTTAAGTCCAGGATGGTGACCTAAACTCAGTTTAAAAATCTTGCC TAGCAGCAC
:ST38775	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGCT/J/TTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
:ST38815	91 C A C A	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACCTATGTGTGTTTCATTCAACAAG TGTTTATGAGAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
:ST38858	98 C T T G A C	CACGAGTAA AAGAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCAAAGTTTGGGGTGGTTCCATATTTGTTATTGTTATTATTA TTCAACACGAGTAAAGAAACTCATGAC/C/TTCTCCTTGGACTCGCTCCTCTCCCAATCTCGAT ACCGACTGCACGTGTG
:ST38865	72 T C T G T G C A T G C	GCTGTAGAAAT TGATGATG	GGAAGGACGG AGGACACAG	CCCTAATGGATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGC/T/CJCTGTCCTCCGTCTTCCCAATAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA

EST38878 9	47 T	AAACATCAATT ACTAGCCTAG ATCCTAA	CCTCAATAAA TCTCATGTCT CA	CCAATGAGAAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAATTCCTGAGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAAACATTCCC TTATTCATGTGTCATCTCACACATTCCTTTATTTTATTTGTTTACATTTCTCAAAATATCGGATTGTTGC TCATGAGAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCATGTGTCATCTCACACATTCCTTTATTTTATTCCTTTTACATTTCTCAAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCACTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCATGTGTCATCTCACACATTCCTTTATTTTATTCCTTTTACATTTCTCAAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCACTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAACG	GGTATTTGTTG ATTCCTCACTT T	GCCTAACTAACTTTTCATTTGTGGATTGCACAGCATGGCTAAACG[A/G]TAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAACACATACACATCAAACTTAGGAAATGTGGTTAGTGGTACGTTGAG GGAACTTATAACCTCAC[A/G]CGCTTGTTTCAAAACACAGCAGACACAGAGATTTCCAACCTC CAGCAATGACAGGCTAGG
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACTGCAATCT CACCCC	TAAACATTCOCATTTGAATTCCTTGGTGG[G/C]GGGGGGGGTGAAGATTGCAGTGTCTCAAGATAAA TATCACAATATATCAAAAACCTTCAAAATTTGCTATGCAATTCACACACTGACATGAGCCACAACACATT CCTTCACAGGGACTGTAC
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGCAGATCCCGACCCCTCGGTGAC[C/G]CAGGCTCCCTGCCAGGCTTGG CCCCGACCGGGCTCCCAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCCTAAGTTCCGGGCTTCCTCAGTCTGGATGGCTGTGGGAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGAGGGGAGGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTG AAAGACCTAACTCTGGA
WI-16398	90 T C	TCCTATTATT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAT	AAAGATAATGTATCATCAACGCAACATATAGAAACATAAAAGAAAAATAAAGTATCCACCCCTAAAAAT CCCTATTATTCATGATATTTTCA[T/C]AGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTGCTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTCATGATTTTCTCATTTCTCATCAGGTTTCTGGTCCCTTTGTCTCAATTTTAAACACTT T/C]TTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAATTTCTCCACAGTT
WI-16406	24 C T	GCTTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCCTTAATGGCTACAGAAAGAGG[C/T]GGTTTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCAATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTTGTTTCATCTGAGAAATAAACTTCCTGTCTAAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAAATGAATGAGGTGTCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGCC	GCACAAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTTACCCACGCC AGCTCTGCTTGCTGCAT
EST39366 2	72 T C		---	AGAAACATTTCTGTCTGATCAGAGGAAGATGTATGTAGAAAAATCAGAATCTGACTGAATTCCTAAA ATCTAT[C]ACACTGAGAGGAAATGAAAAAGAAATGTTTGATAAAGCTTTTCCCTGACTCTCA GAGGGTTCAGA
EST39371 9	86 A G	CATTGGATTAA GCGTGAGAGG TT	TGATTTGAGAC ATTTACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAAATTCCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAAATCAAATGCTTCTCTTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G		---	ACAAGTGACATATCCAAACC[AAC][A/G]TCCATCCCACCTGTGCCCTATTCTTCTTGTTCTTT AGAGCCTTTTCAGCTATTTCTGTGAAGCAAACTGCACGAAGGCTCCCCGTACTCTCCCTGGAA G
EST39428 8	31 C T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTCCTGGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCGCAAT TTCTGGTGGGCTAGGTAATTCGTGCTTTGGTCCACAGAGCACAAATTAAGAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTTGGAAAGAAAATAACAGGAACCTATTTATAT ACGTAATCACTTTTCATACCTGCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTCAATTAGAGGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGGTGG[C/A/G]AGAGGGGCCAGATTGGGTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCT GTAGACATCT	CACCTGCAATT CTGAAGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C		---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[A/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAAGTGTAAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57	A	G	CCTTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATAC/CJ/TTTG
EST40601				GTACCCCAT	TGACCACAAA	GTACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTTGTGAAAGTGTAAATGTGCGGATG
9	78	A	G	GCCTGGAACCT	TTCTTGAAGA	GCTATGTAGACATAAAGA
				GAAACAC	AAGCGTC	TCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTCGCGTGGA
				AGTGATCAC		ACCTGAACAC/CJ/GTACGCTTTCTCCAAAGAGGGCTGTGGGATCAGGCCACTCAAGG
EST41935	32	A	G	ATCTTCAGGAT	GCACACCCCTC	TCCATTGAGTGATCACATCTTCAGGATAGGT/CJ/ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC
				AGGT	ACACTGTTA	AGCTGTGAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
EST43091	28	C	T	CATTCTGGTCT	AAACTGATTT	
				TTATTTTGGG	GTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACA/CJ/TTAGCATGTTTTAACAAATCAGTTTTTCATAGGCAA
WI-18420c	108	T	C	CA	CTAC	CCTTTGAAACATCAAAAGAAATACAATATATTTTCAAAAATTTCTCACTGTAATTC
				TTCCATTAAAC	AAATCTCAGC	AGAGAGACAACAAGAAGAAATAGGGGAAATGGGAAGAACAGAGTGAATTAAGCAAATCTTGGA
				AGGAAGTTT	ATTGCTATAAG	TTGAGATTCATTAAACAGGAAGTTTCTCAAAAAAATCAAA/CJ/GCTTATAGCAATGCTGAGAA
				TC	C	TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA	CCAAGATTTGC	AGAGAGACAACAAGAAGAAATAGGGGAAATGGGAAGAA/CJ/TTAGAGTGAAATTAAGCAAATCTT
				AAATGGGAAG	TTTAATTTAC	GGATTGAGATTCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
				AA	TC	TTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	---	---	AGCTGATCAGCTGTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCTGTC
				CACCTGTCT		CTAGACAGATTCA/CJ/TCACACACAACAACAGGAGGTGGGGTCAACACGGGGAGAGCCAAAGAC
				AGACAGATT	CCTCCTGTTGT	TAGGGC
WI-18425	81	A	C	A	TGTGTGCA	AGCTGATCAGCTGTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCTGTC
						CTAGACAGATTCA/CJ/TCACACACAACAACAGGAGGTGGGGTCAACACGGGGAGAGCCAAAGAC
						TAGGGC
						AAATTGAGGTCCGGTGGAACTATAAAAGGAAAGAAAGAGAAAGTAATCAAGGGAGGCCAAAGTG
WI-18449	129	C	T	CTTTGGCTCT	CTCCCCTGACT	GGAAAGCTGATTGCTGATCTAAGCTGCTGTTCCAGTCTCTTTTGGCTCTAAGTGGGACTA/CJ/TTTC
				AAGTGGGACT	GTATCCAGA	TGGATACAGTCAGGGGAG
						ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGGCCCCCAAGACATTATTTTATCTT
WI-18457	120	T	C	---	---	AAATGTCCAATATCTGCCCTGATGTGTGTTTGTGCACATTGGGGCCACAGT/CJ/AAATAGGCTAAA
						AGGCAGTCCACCTGCT
						GGTGCTATAGCTGCTGTACACCACAATGGCAGAGGTGA/CJ/ITAGAAACCATCTCAAAGCCTAAA
WI-18462	39	A	G	AGAGGTGA	AGATGTTTCT	TATTTACCATACATCCCTCACAGCAAAAGTTTGTCTCGGTTTAGGGACTCCATTGAG
						TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGCTGAGGGTGGGGTGGGAGG/CJ/TTGGT
WI-18476	60	C	T	GAGG	GTGAAC	CATCCCATCGTGGCCCTGGCCGCTCCCTCCACTACCCACACCTGGCCAGTCCACGTTGAGGT

MI-18491	109	G A	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCITGTAATCC	CTAATGAGATGAATACATGGAAGCGCTTTAGCACAGTGCCTAAAAACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA CGT
EST50757	79	C T	GAGCTCGAGG CTGCTTCT	ACCCTTCAACC GACC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTTCTTTTATAT GTGACGGGOC[C/T]GGCGGGTGAAGGTCAGAGA
WI-17675	103	T C	GGACATTTGG ATGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAAACTAAACATCTTCCACAGGTGCTGAAGAAAAAGTGCTTCCGTTTAAAT TGCCAAAGCAGGATGTGGACATTTGGATGGTACTT[C/G]CCTGGGTGGTCCCATAGATTCAACCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTGGGTTT	GATTCATCATT ACAGGGACTT	GATCCATTACCTAGGGTAAAAATTCCTCTGAATGTCAAAACAAAGAGATAAACTACATTTGGTTTGGT G/TJAAGTCCCCCTGTAATGATGAATCAAGAATCCTCAAGTCTGCTTGGCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGATTTCATCCCAAAACCATCTCCCTGACCCCGAGTCCATGGAATAATTGTC TTCCACAAAACCGGTCCCTGGTGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTGGTACAAAAAGTAATT G
WI-17690b	79	A G	---	---	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTATT[A/G]GATTACAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGAGGCAATTTTCTAGCTGTGTTT[G/A] TTGGCTTCCCTATAGATTACAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGCTTAACATCATCCAGATTATTCTGAAGTGGAACCAACCCCTCCGACCCAA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCTCAAA
EST51717 a	39	C T	---	---	GATCCAATCTCAGTGCTTAACATCATCCAGATTATT[C/T]TGAAGTGGAACCAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCTCAAA
EST53012	97	C T	TGGTCACTTTG GGGOC	GGCTCTGCCCA GGOC	TTCCAGGTTGACAGGTTTATTCCACCCCTTCCATCCCATGGCCACCCCGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGGAGAGCCCACTGGGTTTACATTCTCTGT GGGCAGGTTGGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTACATT TT	AAACTGCAAAATAACAAAAACAGAAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAAAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAA CA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAAGGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAAGGGAGATGGCC

[illegible]

[illegible]

TIGR- A003P30	117 C G ---			ACAAAGTTCAAAGGAGAACTTCCTTTGTTTTTAATGCAGCTGTGCTCAGAAAGCCCTGTGATTTCCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A			GCTTGCTTTTATGTTTAGGTTGGGGGAAAGGAAGGGCTGACAAACCGCAGACATCTGGACACCAGC AAGGGTCCAGGGAGGTTTGAGAACTTCCTTTGCTCTGGCTAACAGTCTGTCATGTGACAATAGCCA AACCTCCTCATTCCCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---			AACAACAGTGTAAATCTTTAACAGGGGATGTTAAAGGTAAGTCAAGGAAGATAAACCAAAATGAT TGAGTATGATAAGAAATTTTGCATGGCGATT[C/A]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA			AACAACAGTGTAAATCTTTAACAGGGGATGTTAAAGGTAAGTCAAGGAAGATAAACCAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAAAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCTT			CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAAACAGGCATTCTCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTTT AGTAGCTGTCAAAATTTCAA
TIGR- A004V26	125 A G ---			TCTAGCTATAAGACCAGATTTTAAATATCTAGATATAGAATTAATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 3	29 A G CGATCTC			CCAGGCTATAATGTTGGTGCGATCT[C/A/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAATTTTTG TATTTTITAGTAGAGACATTGTATTTTITAGTAGAGACAGG
TIGR- A004X20	25 T C G A			TAAGTTTTCCCTTCCTCTGTAGGA[T/C]GTCTCCATGTTACAGTCAACTATAAAACATGGCTCATGT TCACCTCGGGCTTCGCTCAGAGGAGTTGATATTTGGGAAGTGGTACCTTTGTTCTGIGCTTTTCA GACCAACCGCTTCTTCAATTTCTCAAGGCTTCCTTCCAAAGGAGTTAAATCATCATGTCCCAATC ATCATCATGTCCCT
TIGR- A004X30	26 T C CCAC			TTTTGAAATCTTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACTGTAAATAAAATTAATAAGTTTT AAACACTTCCATAAAGAAATTAGGGTGCCCGAGCTCCTTGATTTCCCCCTAGGGATAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT			CACGGTATATGCCTTATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[T/G]TTGCTTTCATGAAATTTCTAAATTAAGG ACTGTTGCTTCTTCATATTCATATGACATTAACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGATTATTGGAGGAGCTTGACACCCCTCTCTGCCCTAGCTTGAGAGAACAACATGCG AGCATTTTTTCTTTTTC/TCTCTCCGATGACCATCTTTGGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCOG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCCAAGGCCAGGTAGCCTTCAGGGGGGGGCA GGGTGGGGGAGGTAGGAGACTC/TJGGACCGGAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCT/CJGTCTAGATCTCTTGGCCTCTCTGTGCAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG/CJGTCTAGATCTCTTGGCCTCTCTGTGCAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGTATCTTACGACAGTCAAACCTTACGACAGTCAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTAAAA CTGTTACAC	TTGCTATTAT TTAAAGCCAAC AAAA	CATCAGTAAACATATACACAATTGGTCATCAACTGAACCTTGCCTCCAATATATTCTATACAATCTT AACATTATTGAACCTTAAACCTGTTACACT/G/TJTTTGTGGCTTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAGTGAATTAACCTTTGTAGACAAGTGAATTAACCTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCCAGGCCCTCTG/AJCTCACAGCTGTACTGGCTAGGCCAAAGCTTTCCAGAC ACAAAGCCACCTGCCCTGCCATGTGGATAGTACTCTTGGCTGCTTGCCCTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAAAAAATTTGTTTAGGGAAAAAATAAATCCAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGCTGAGACAGAATGACCCCTTGGCTCCTTTATTTGTTCTTTTCAACAGGACC CCACAGATAATTTGCGGTATGTCATGAGGACTGGGATGCTTCTATTG/CJGGATGCTTCTATT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTACTGCACCTTACAGAG/GJCTCAATTTCCCTGATTTAGGA AGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTATTTAAGAGAATCCCAAG CTTGGTAAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTCGGTATCAGGCACCTGACTCGG TGCCTTTAC/GJTTACATTACCTCACAGCCAGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTTCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCCCTGCTTACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCCCTTGATATTGTAAAAATTCCTCCCAAGAGCCGCATATGAATCTGCC

X57830	106	G C T	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTCGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG/CJATGCCTCATTTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAAATGTGCTTGAAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G	CTTTTAAAGAA ATTTTGTTTA TGGATC	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATC/TG/GJGATAAAATCTAGATCTCTAATAATTTTAAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTT CAGTTTTTGTCTTATACACAATTCATCTTTGCAGCTAATTAAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T	---	---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACCAAG/C/JTAGAGCTTCTTCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTTCATGCACACACGTTGTGAGATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAGTAAGTGAAGG TCCA
D28513b	133	A G	---	---	ATGACCAAGCCACACATTTAGAACCTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGC/A GJTGCGTGCAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	---	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA/A/GJTTCTCCAACGTGATCTACCTCCCTACTCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAACCAAGACACCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D29833a	21	A G	---	---	CCACTCCATCCTGATGCCCCA/A/GJTTATCCACAGCCTCCTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCCTCAACTGATCTACCTCCCTACTCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACCAACCAAGACACCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D31762	82	G A	---	---	CTCCCTGCCTCCTCCTCCTGCCTGTGATGCTCCGTCTCAACAGCCGAAACCTGTCTTGCAATGGGG GAGGGGGCGTTTC/G/AJCTTTCCCTCTCTTGGCTTCCCTTATCTTCCACAAACCATTCCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64	T C	---	---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/CJ CCCAGGCTCTGTCTCCTCAGCTCATTTCCCTACTCTTTCTCTATATACTCATCTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAAGCTTCC TTT

D63807	101 C T ---			CAGCAGGACTTCAGTGTAGTATCCCTGCCTTCAGTCTCTTTAGAAATCACATCTGTGTCAATCC ATTGTTAGAGGAGTGATTTTCCTGTTCCA[C/T]GAAGAGGAGACTTTTGTTCACAATTTGGATCAC AATGCAGAGGAGTCTGTCTCCCTCCCGTCGGCTTCTCGGTGCTGGAGGGTGACCTGTCCAGATGAC TGGGAACATGCGTGTGACCTC[T/C]ACAGCTACCTCTTCATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTCTTAACCTAAATTTTAAATTTATTTATACATTTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTTGTGATTTGCTCTGAGAGTTCCCTGTCCTCCACCTTCCCTCAGAGTGTG TCTGGTG
D90145	21 T C ---			ATTACACTCTCAAAAATTTGGTGTGTGTTTAAGTACTTTCTTATTTATGAGCCCTT[C/G]GAGGA CCAGACATGTTTATCAAGCCCTTATATACCATCTAAT
EST14035 1a	59 T C ---			GCATTTTAAAAATTCACATTTGAATCATTATTACTATTATGATGTTTACATAACAATTCAGTATCATT ATG[C/T]GTAGATTTACAGATGAGTCTGTCATCTGAGCATTATCT
EST16904 7	71 C T ---			ACAGACTATCGCCAACTTATAATGCTTAAACTTTATGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTATTATAAAATAGGGTTGTGTAAGATGATTTTCCCAACTGTAGGTTAACAT
EST21863 9	57 C T ---			TTTTAAGTACCAGAGGCACTGCTGGAACAGGATGAAAACCTGATACACC[A/G]GTTACTACTTACTC TTCACCTCTCAAACTGATCCCTAAAGACTTCTACTTAGCAA
EST21885 6	49 A G ---			GGCTGTAAGTAGAATCAAAAGTTAAGAACATTTTATGCACCTTATCCACAACATTTACTGAGCATA CTAGGTGCTGGG[A/G]TGTGACAGTGAAGCAAAAAACACAA
EST22623 3a	80 G A ---			ATTTAGTGCAAATGACAAAGCCCAA[A/G]AGACAGAGGATCAAAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACACAGTATGGGAGT
EST22644 2	26 A G ---			AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAAAACAGCACTAAAAATAA AAATTTTAAAAATGATTATCCATTATTACAG[A/G]AAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	98 A G ---			CCTCATTATTAAAAAGACGGACATAAAAA[A/T]ATATACAACAAAAACCCCAAGTCACATTTTCAG GAGTAAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	31 T A ---			AAAGATCTGGCATTATTCACATCATTCTAAATATTTTGTAAATTACTTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC[T/C]GAATAACCCATAGTTACAGAAATTGG GTCTGTGTAACCTCAATT
EST24308 3	106 T C ---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAAATATAAACCTCGTTC
EST24435 6	45 A G ---			CTTGAACCTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC[G/A]TGCTGACCCACATTTCTTTATCCGATCTGTTGATGGACATTCAGGTGTGTTTC
EST25089 6	73 G A ---			TATTGTTGCATTATCAAAATGGTTA[T/C]JAGTTTCAATTAAAACTGTAATTGATTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAACTCGTTAGTTAATGCTACATT
EST25089 6	25 T C ---			

EST33508 1a	36 A G ---			AAAAACATGCTATTTGAACAAACTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAAGCAGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTTATCTTGGTTTTGAAAAATATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAA[C/T]TCTTTGAACACAGCCTGAATCCCCC
EST34739 3	97 T A ---			GAAGTATCCTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC[T/A]GGTGCCCTTACAACCTCCAACCTACTGCAGAATTTCT TGTTGGCCTCATAAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAAGCTCTTTGTAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATCTTAGTCCTATTACA AAGATTTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTTGCAAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTTGCAAAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGCTTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGGTCCACTTTACTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCT[G/T]GCCTTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			CTTTTCAAATTTTGTAGTGGCATTATTAATG[C/T]TATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTTGGGCATGTTGTTCCATTTTACTTAGTTTCAAGAACTTTTCAATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACCTTTAGGCAAAATGGAAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTTGCTTCCCTCTCTGAGGTGGCACCTTTCTCTGTTGTG ATGTGCAAAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATAAACTGAGGGAACAACGGTGTGACATGGCAGACATTTTATTTCAATGGAGA AGTTCTCCCATGAAACCAAGA[C/A]CTTGCTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCTGTGA
EST36301 4	93 C T ---			CACCTGTTCAATTGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTCAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 2a	33 G T ---			GCCATCAGCCCCACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGCACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGTCTTAGTCGT

EST36620 6	50	G A	---			GAC TTATTAGATAAGGGTTTCGGGTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTATTTAAATATGGGAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89	C G	---			CCTGTGATGTCATGGTGCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCACGTATGTCAGGA AAGGAAGTCTGGGATTCTC[A/C]GJAGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62	C T	---			GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCCTCTCCTCTAAATATACTGATTGACAATG[C/Π]A TATTAGCCAGGTAATGCACITTAGCTACCTCGACAAATGCTATCAAGTGTCTGGGAAGGGAG
EST36823 6	103	A T	---			ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/Π]TCTTTTATGTTCTCCTAAGCTCATCATGAG TTAA
EST36987 4	126	C G	---			ATGATCGCTTATGTAAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88	T C	---			GGTCTCACTCTTGTCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTGGTTTAAAGTAACCACCTGAA C
EST37269 3b	105	T G	---			AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTTGGGATTTTAAATTAAGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTTGAAAGTCT[G/C]CAGGAGAAAAAATGGGGTCC
EST37284 2	93	G T	---			AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTGAAGGATGAACCCAGGAA GCTCTCTGGATAATGTCACCTCTAGGAA[G/Π]AGTAAACAGGTTTAAAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCCTGAGGAATA
EST37315 2a	90	A G	---			AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACCTAAGATATCTCTCCTCAGCCTCCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45	C T	---			CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/Π]AAGGGTGAAAAGCATACC ATTCCATTTTAGTTGAAATATTCTTCACATAGCCCAACACATTTTTC AAGGCACTCTAGCTACTACA GGA
EST37376 8b	101	G C	---			GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGTTCAGCGCTGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTGCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41	T C	---			GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAGT[C/Π]GAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTCTCTCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAAACCTCAATTCTGTGAAAAACIT/G JAACATGCCTCAAAAAAGAGGGGAAAAAACCTTACAGAAAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAATCTGCAATGAAATCAGTTATGAATATTAACCTCT[G/A]CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTTACC[G/G]GTCATGAATTCATTTAAAAACCCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAAATCACCCCTGGTTCAATGGATCTTCCATTCTAA
EST38025 4	56 T G ---			TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTATATCACCTTA[T/G]TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGTCTTAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTA[C/T]JGCAATGG AAGAACGCTCTCCTTTTAAATCCCTAACTCTCTCTCTGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCTCTTTTCAATTACCAAAACAAAAAAGGGAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGTATCCTGACTGAC[T/C]GTCCCTGCAGTGCCCATGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25 T C ---			TTTATTTGCAAAAGTAAGCAGCCGG[T/C]TGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCTG CTGGAATACTTGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 5	90 T C ---			TTTTTGTACTCTGTAGCCAGTCATTAATCTGAAGGTTTAAATATATCATTTTATTTGGGATGAGATCA TAGTCTTTACACAAATGCTATG[T/C]AAACAAGTTACTGAATATTTTTCACCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCTTCTGCTCTAGCACTCAGACCACCAAGAAAGCCTGGAAGACCAGCCATGGAAGGAAAGTA TG[C/C]GTGTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---			GTCACCATTGACCTTACATAGTGCCTCTAGT[C/A]ACCTATGAGGCACCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTCT[C/T]CAAAATAACTGAAACTAAATCTGT AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTTTCCAGAAGGCTCAAGGTGTTT AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTCTAGAGAACCTGTGTGATACACTACGCATGCACA[G/A]ATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCACTTTTGAACCTAGTCCCTGCAAAAGCACCTTCTA CCCTGCACCTTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCTTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAAA[A/C]GGACTTGGAGACAGCGATTAAATACGGAACAAGGCTCTTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGGTTGTAGGAATTTGGGAAGAAATTATCTGTGAAGGAAATTTGCCACTGTAATGCACACCC A[A/G]TCTGTACTCCCAATATCCTATGTTTAAAGCT

51	G A	---			GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
134	T C	---			CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCCATCAT CCTCAGGCCCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA T/CJTTCCTTGGTCTCCAGTGGAAGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
63	T C	---			CTGAACCTCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTCTCATTCTGTGAAAACTA[C/T]CJC CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
69	T C	---			TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGOC C[T/C]ATCCATTAGTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTCTGTCTATTGGATGACTTTGAGATTTATCTTTGTTTCTCTGTTGGA ATTGTTCAATGTT
36	T C	---			GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAG[T/C]CTCTTGTCTGGACCCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAAGAAAGGCTTTGGCCCTGGTGTGGTGCATAGGCCTGTAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
137	G C	---			GGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGAAGGGCAACACCCAGCGTCCCCAC CC[G/C]CGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
123	T G	---			ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTAGTTCTTTTGTATTTGTATATTTGTCGCTGA AGATCATCCCGAAGCAGGCTGGAGGTGCCGTGGGCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
173	G A	---			CAAAGTTGTCTCTGCCCATGAGCACACAGTCAGGCCCTTGAGGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTTGCCAGCTCCAATGTACAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACCACCAAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	AAGTGACAGAAAGCAAGATGGATTGTTCCCTATAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAAGCTGGAAGAGAGCTCAAGTTTTTGGTTTACTTTTCAGAAAT/CJGAAAGAACTTATTTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAAAGTCTCCTGTACCTTGAGATCCA GTC
M18079	52 G A ---	---	GCGCACAGTCCAAAATACAAAATTGGACAGAGATCTATATTGTACCAGAACT/GA/JTTTATTTCACC CCATCAAGTATAAGGTACTGATTGATTGGTCTTTTATAAACATTGGTATATTCCATTTCATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	TAGGGATCTGTGCCAGGCCATTGCGCACCCAGCCACCACCCCTCCACCCCTGTAGTGTCTCCACCCC TGGACTGGTGGCCCCCACCTGGGGAGGCCCTCCCATGTGCTGT/CJGCGCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTGCTCAGCAGGGCGCTCCGCCCTCCCTCTCTCTCTCTCTAATA GC
M21539	114 T G ---	---	TCACCTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGCCCGACAGCAAAAT/GJGTTTCTCTCTCTCACCTCT CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCTTTTCAGAGCT TCTCTTGGGTGC
M26041c	173 A G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGACTTAAATTCGTATATCTGCTCAGAGCTCACAATGCCTTTGAAATTAATTCCTGACTTC CTGATTTTCTCTCTCAAGTGTACCTACTAAG/A/GJGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTCCAAATGTTTCTCTCACCTCT TCTGTGGACTTAAATTCGTATATCTGCTCAGAGCTCACAATGCCTTTGAAATTAATTCCTGACTTC CTGATTTTCTCTCTCA/A/GJGTTTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCCTC/GJCAAAATGTTTCTCTCTCACC TCTCTGTGGACTTAAATTCGTATATCTGCTCAGAGCTCACAATGCCTTTGAAATTAATTCCTGAC TTCCGATTTTCTCTCTCAAGTGTACCTACTAAGAGATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	TAGGCAGCTGTCAAGGGAGGCCAGTCAGTCCAGCAATTCACAAACCCTTGAC/GJCAATGCT TGCCAAGCTGTTTAAAGCCAAGAACACCCCTTCTTTGTTCCAAATTAAGTCTTAGAAGAAACCCCA CAATAAAGCAATTCATC
M81695	34 G A ---	---	ACTTACTACCCCTCAGCTGACGGGGA/GJGAACCACTGCACCACCGAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAAACGCTTGTCTGGGAAGGGCCCTTGTCTTGTCAAGGTTT CAACTGGAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCCAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	C T ---			CTCCTCCTTTATTTTCAGCATGGAGGGTTTAAATGGAGGATCTCCTTTTCTGTGACAAAAACATCTTTC ACAACTTACCTTGTTAAGACAAATTTTAAAAAGATCTTTTTCACAACTTACCTTGTGTTAAGACAAAATTT TATTTTCCAGGCTATTTAATACGTACTTTAG[C/T]TGGAAATTTATCTATGTCAATGATTTTAAAGCTA TGAAAATACAATGGGGGA
U09607	39	T C ---			GAGGCCTTATGAGGGTCTCTACTTCAGGAACACCCCAAT/C/GACATTGCATTTGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGCAG TGGGCTCTCTGAGTCTCTGGCCCAAGAAAGCAAGGAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C ---			GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC/T/CACATCTGCCGCCCTTCCAGCCCTTCCAGCCCTCCTCTGTGTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20	C G ---			GTGACATGAGGCCCATCTT/C/GGCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTTCCTTGCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAATGTTCTTTTAAATGGTCAGTTAATGAACATTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C ---			AAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAAC CTCTTTGTTTCAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAAAGAGAT/C/GTTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	T C ---			TTTCTGTCCACTTTTCACTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTTGAAGAAATTAATAAGCAATGCTGAACATCAGGAATGTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG/C/TJGGTCTCATAC CTCATATGCAGGATTCATCA
U17077	122	T C ---			TCCAATTATTGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAAACAGAACGTCCTTGACACTGAGCGATGACACCACAC/C/TJTTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58	T C ---			GCACATGCAGAAATAGACTCAGCCCTATGTCTGATTCCAGCTGGGTAGTCTAGAACTTT/C/JAGAAG CTCCATCTTTTAAATGTTTATTTGTTATGTCCCCCTCCCGCTCCCACTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACTTCC AAGGCTTTAGTAGAGAGGCC

J25975b	164	C A ---	---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTAT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAGCAATGACTATTCCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
J25975a	143	C G ---	---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCTTTTAGTATATGAAAAATTAT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAGCAATGACTATTCCTCTG AAGACAAC[C/G]AAGAGAGAAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
J25997	61	A G ---	---	---	CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCCTATTTCTATCCCCCTTAAAGAAAAAT GCATGAAACTAGGCTTCTGTAAATCAATATCCCAACATTCGCAATGGCAGCATCCCAACCAACAAAA TOC
J28413	29	C T ---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCCTCATGTTTAAAAATGAGGTT AATATTTGCATAAAATCCTAAAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAAGTCGTTGTACCCCTCAGTT G
I30884c	89	A G ---	---	---	TAGGGTAGCATTTAAGATTACAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGATGATGATGATGATGATGATGATGAT TGACGGAAGTCATTAGAATGGCTTGTAATCTGATGGCTTGAACCTGCCACACAGTTGAACACAAAGT GCTGTCA
I30884a	34	A G ---	---	---	TAGGGTAGCATTTAAGATTACAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGATGATGATGATGATGATGATGAT TGACGGAAGTCATTAGAATGGCTTGTAATCTGATGGCTTGAACCTGCCACACAGTTGAACACAAAGT GCTGTCA
I31216b	78	A G ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTCAATCA[A/G]CCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCTTTAGCCCCGCC TGGTAGCCCTTCCAT
31216a	70	G A ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC[G/A]TTCATCAAAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCTTTAGCCCCGCC TGGTAGCCCTTCCAT

U31416c	76 GA ---			AGTTGCCAGCTCCCATGTACACAGAGCTGGAATCTGAAGGGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAQ[G/A]CCACAAATCTGGTGCCCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCT GGAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACTTGACCCCTGCCCACTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT ---			AGTTGCCAGCTCCCATGTACACAGAGCTGGAATCTGAAGGGGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCACGCCACAAATCTGGTGCCCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTTCACTTGACCCCTGCCCACTCTCCCA ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---			ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCACTCACATTGTTCTCC AGACCGCAGG[C/T]TCCCCCAGCCTCAGTTGCTGGAGCTGTACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGACGCTGCTCGAGAGAGCGGAGAGGCCGCGCAGAAC ATGCCAGGTGTCC
U37690	54 AG ---			GACCACGCTGAAACCCACCCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[AG]CCCCGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGAGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGTCCTT
V00540	39 TC ---			TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTATAACCCAGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCGAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT ---			TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCTAGAATTTGGATTCTCTGTTTTTTCATGCTCTCTCTT GTAACCCCTGAGATCATCAG
X52011b	148 CT ---			AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGGAAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAAAGTTGCGAAAAATGCG AAATCTGTTGTGCA[C/T]GCTCAAAATGAAAAACGCCCTTTCGGCTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 A/C ---			AGGAAGATCCCACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGGAAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAA[A/C]GTTGCGAAAAAT GCGAAATCTGTTGTCAGCTCAAAATGAAAACGCCCTTTCGGCTTTTGGCTTTATTTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGTCTCTCTCCACAC[AG]TGCACAGCTTCTGAGTCAACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCCAGGGCTCCAGACTGGGCTTGCCAGGCTTGCCAAATAGCAAGGCCAG GGCAGCTGGAGACGATCTTGCTGGCAGGGCTGGCTTGCCAGCCACCTGGCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATGTTATTTGCTCT[AG]TACAAAAATCTAAATCAATATTGAAATAG GATGCACACAATTACTAAAGTACAGACATCTAGCATTTGTGCGGCTCATTTTGTCAACATGGTA GCCGTGCTGACACCTCCAGAACGAGGTGCTGGGCCGTTCTGCCCTGGGACCCCGGAACTCTC CTGCCGGAAGCCGACGGCAGGGATGGGCCCAACTTGGCCCTGCCACTTGACTTCAACCAATCCCT TCCTGGAGACT[AG]AACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGCGCTGAAGAGCCAGA GAAATGTGAAGAATGTGACAAAGCCTTTAAAGCGTTGTACACACTTGATTGTATATAAGATAAT[GT]GT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTTACTTGAGAAAAATTTGATAAAGATGGAAGATCAATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X78932	62 T G ---	---	CTAACCCATAACCTCAACCACATCT[CT]ATCTCTCCACCCACATCCCACACATCCACCTCCATCC CCAACCCATCTCATCCCCAAGTAGAGCCCCAAACCCAGCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCCAAGTAGAGCCCCAAACCCAGCCAGGCTATCCCCAACCCATCCCCAAGCC AACTCAACAGCATCC
X80026	25 T C ---	---	ACCCAACTCAAGTCCAGGGCCCCAGGCATCTTCTGCCCTGCCCTGCTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTCTAGCTACTTCTCT[GT]GCTTTGAAAGACCCCTCCACTCTCTGGCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG ACCCAACTCAAGTCCAGGGCCCCAGGC[AG]TCTTCTGCCCTGCCCTGCTGGCCCATCCAGTCC AGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCTGGCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG GGCAGCCAGAGTGACCAAGTCCAGAGGGGCGCGCTCGCGGTGTCGTTTCTTTT CAGCCCGGAGAGTCTGACCTGGGGCTTCTCAAGCCTACTCGCCACGCTCCCGGCGCTCT CTTTTCTCCCAAGC[AG]AAACCAATGCGCCCTTACCTCGCTGCGGCGGAGGCGGGGCTT CTTTCAGAGC
X80197a	28 A G ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTCCCCCAGACGTGTGACAGGGGACCCCTCTGCC CACTCTGGCTTTTCAGATACCTGACCAAAAGCCTGCTTTAAACCGCAAGATGGGGCT[GT]GGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACCTGTCCAGGCTGAGATAATCCC GGGA
X80197b	99 G C ---	---	
X85106	150 G A ---	---	
(87160	128 T G ---	---	

1282	130	CT ---	GTGCGATCACCACACTACAGTCTAATTTTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTTGTACCCATTAGCAATTAATTCCTCATTCCTGCCCTCACCCTCAGGCCCTACTCTTTATCGCTATAGATTTGCCCTCTACTTGACATATACACATGGAGCCATACATATGTGCCCCCTCATGATTGGCTTCTTTCACGTGAGATAATGTTTTCAAGGT
6810	68	CT ---	AGTATCACACATACCTTAATATATTAGATATACACAATAATAAATCACTCCCTACCTTGAAAACCTTTA/C/TJAGAAGCATTTTTTAATTTTACAACACAAGCTCAACAGAACCTACAATAAGTCTAGTAGTCTGTTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTTAAAAATGICTATGAACAAGTACAAATTTCTTTTGAAGTCTGCAGAGCAATGACCACCTAAGAAATATTTTAAAGGC
6817	118	AC ---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC/A/CJTGTGGATACCCCTGTGTCTCTACTGGCTCCAAAGGCATTCAAGGGATCATCAAAAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCTGTGCAGATCGGCTTTTGGTTTGGTTGCTTAG
3819b	212	C ---	CCATTTATTTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCCCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGCCTTTAGCAAA
819a	166	GT ---	CCATTTATTTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAGCCTAGTAAAGCCCGTCAGTAGTACACATTTCTCTATGGTCCCTTCAACAGTTTGT/CATATACAAAATTTTCTGCTATTTTGCCTTTAGCAAA
81xx	39	AG ---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTJA/GJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGACACCCAGCAATGTCCCTTAAGATATGCAGCAAGCACAAATCTGTCTATGGTTAACAAAAGAAATGAACGTCTAGG
972b	149	GT ---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCCTTGACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAACTATTGATTATTGCCACAAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTCTTCTCTGTTAGTCTTGGGA
172a	122	AG ---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCCTCCTTGACCTCTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA/GJCTATTGATTAATGCCACAAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTCTTCTCTGTTTAGTCTTGGGA

598k	210 A C ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTTCT CAATGCAG[A/C]
598j	208 A T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTTCT CAATGC[A/T]GA
598i	192 G T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTTCT CCTCAATGCAGA
598h	144 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
598g	142 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
598f	120 A G ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTTTA TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
98e	83 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGCCGCTAA[C/T]CAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA
98d	77 C T ---			AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTTATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCTT TTAATAATTTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACA[C/G]CCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCTT TTAATAATTTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATT[A/G]GATTTACAAAAGACACCCCAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCTT TTAATAATTTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTATCTTCAAGGTCCCCAATA[A/T]CCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCT[A/G]CTTCTCAAGGTCCCCAATAACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTGCCAGCTCTCCTGTA ATACCTTAATGAATGGGTGATGCTCTATCTTCAAGGTCCCCAATAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTAGAAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAGCTAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCAATTTGTTAATCACTGAATC TGGGTTTCCCTCTGAATTCACACAGAGCATGCACACACATTTTATCAT
9467b	93 C T ---	---	AAGGCTTTCCCTAAACATCAGTCTACGGAGAAACCTGGGAAATCCTGGATATTTGGCTTATCATT TGACGCAAAATCCACTTTGCTGTA[C/T]GGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
3467a	70 A G ---	---	AAGGCTTTCCCTAAACATCAGTCTACGGAGAAACCTGGGAAATCCTGGATATTTGGCTTATCATT TG[A/G]CGCAAAATCCACTTTGCTGTGTAACGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8498	84 C T ---	---	AGGGTTCAAGGTTTGGTTTTAAATCAGGCTGCACACCTTTCAAATCAATCTGACATCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACTTCAATTAATCGAAAAAGAAAAAATTGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCCCTAACTCAG

WI-18562	29 GA ---	---	CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51 AC ---	---	ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTCCCTTCGATGCAAAAGTATAATTGTAAACCCACAGTGCTCGCACAGTTC AC
WI-18683	22 CT ---	---	TAAGCTGTTCCAGGACTGGACT[C/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75 GA ---	---	GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCTCTTCGGTGAGAC
WI-18563	94 AG ---	---	AAATAAGTTTTATTGGCACACAGCCCAAGCCCACTGGATGACACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAGCCAAAGATATT
WI-18582b	69 TA ---	---	GTCTATTTTCAATTTAGCTAGACCCCATTTTCATCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCAG
WI-18723f	94 GA ---	---	AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGTAACAGGTACATAGGTAACCAA[A/G]ATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71 TC ---	---	AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGTT[C/A]ACAGGTACATAGGTAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96 AG ---	---	AACITTTATTTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGCTGTAGATTTTGAAG TGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44 GA ---	---	TTTATTACAATATTTAGGTGGCACAAATAACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACTCGAAATA
WI-18715	76 GA ---	---	TTATCACAAAAAGTGATATTGCAGAGGGCTGGGGCTGTACATGGGCAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGGTATTTTAAATAAAAAATAA TGGAGCTACAACCAACCC
WI-18535	107 GA ---	---	GTAATAAAGTTTTATTGGCACAGCCACGCTGTTTCATTATGCAATGCAATGCTGCTGTTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGGTCCCGCTG
D17525	107 CT ---	---	AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGGCAGGTGAC TTCATCTCTCGAACTTCAGTTTCTTCATAAGATGGAA[C/T]GCTATACCTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTGTCTACCAGGCAGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAITTCAGATCATGAATGACTGACAGAAATTTTGTGGGAGTCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACCTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAITTCAGATCATGAATGACTGACAGAAATTTTGTGGGAGTCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACCTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCTTATTTATTACAAAACAGAAATGCTCATGACTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAITTCAGATCATGAATGACTGACAGAAATTTTGTGGGAGTCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTGAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACCTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTTGTGGTGGCACCCTCCTACGTCACATGAAGTG TGTTCCCTTCAGTGCATCTGGGAAGATTCTACCTGTTGACCAACAGTTCCTCAGCTTCCATTTCGCC CCTCATTTATCCCTCAACCCCGCCACAGGTGTTTACAGCTTCTTACAGCTTCTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTCTCCTCAACATGGCTCACAAATTTCTATCCCAAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCAGTCCCAACAGTTCATCATATATAAGCATTATTTTAA CTCTTTTGAGGTGAATATAATTTATATTACAATG[GT]AAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAAAGTAAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	--- ---	---	ATTTAGTGCTTTGCGTTAAAAAATCATTGCAAAAGTATCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTAAATGCTTTCTGTTAG GCCTTCTTCTTACAATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTAGTGCTTTGCGTTAAAAAATCATTGCAAAAGTATCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA[AG]ATCACTGTAATTAATTAGTTTATTAGAGCACAAGCTTAGCTAAT CAACCATTTATTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTTAGTTAAATGCTTTCTG TTAGGCCCTTCTTCTTACAATGAAGAGATGATCTTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAATTCAGTTTTTTTCCAGTTCCTCTTTGTGCTGCTTCTCAATTAAGGTTAGGTC[GT]AT AAATCAACTGTCCATCAGGTGAGGTGCTCCATACCCAGCGGTTCTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	TCATACTAGGCGAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATTCCTATCACCATACAAAAATTTA ATJGCGAGTATTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAGTCTGAATTTATGGGTT CTATGCATGATTTTGCCTAACCTAGAGAAAGAGTTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	AAATCCAGGCATTTGCAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAGTGCCACTTATTAA AGAGCTTCACAGTGAAGATGGAGAAGGTGAACCTGCTTTGAATATCCAGATGTGTTGGTC[A/G] TGCGTATGGCAGTGAGCAGGTATGTTGCTTTTGCCTTGCACTGAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTTTATCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	AACTGCATATAGATAATTATCCAGGATGTGGGCTCATTTTCAGCTTGTCTTCTACTGTTTGT ATATACAGTTTTTGTAAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAATAACATATCTTGTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATCTAGTCTGATTTCG
DWU-59	94 C T ---	---	CATTTCTTTGTGAAGGTAATGGACTCACAGGGGAAGAAACATGCTGAGAATGGAAAGTCTACCGG CCCTTTCTTTGTGAACGTACATTTGGC[C/T]GAGCCGTTGTCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAGGTGTTTTACTTCTGATAGCCGGTGATTTCCCTCCTAGCAGACATG CCACACGGGTAAGAGCTGAGTCTGAGTCTGATTGTTAAGC
EST11	68 C -- ---	---	CTTGATCATGGGTGGAATTTTGTGTAICTGGGCTTCATGGGATGCAATAAAATTTCCAGTTGGTAAG CAGCAGGTGCCGAGGCTGCGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	CACACTGGCATCTAGGCCCTTCGCCTGCATTGCAGAAGGAGAGCCAGGTCCCTCCTGGAGAA[C/T]G CTGGTTCCCCAGCCCAACCGGCTTTGCACACACAGGCTGTGAGGAGGAGGTGGTAAAGACGT AGCTGTAGACCCAAAGCAACACCCAGCCCTGGACCCCTGCGGAGAGGAGCAGCTTTAGAACATGGAA AAGTGTGGTCATCCCATCATTAGACAAGACACATCCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGT GTAATTAGGCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAAGTGGCTTCT A
WI-18036b	97 T A ---	---	TTCCAATGTAAGAGTCAAGTACCAGTTAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
NI-8036a	27 T C ---	---	TTCCAATGTAAGAGTCAAGTACCAGTT[T/C]AACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
VI-18046	72 C T ---	---	TGTAAGGTGACTTCTATAAGCTTCCTAACTGTCAAACCTTTCATTTACTGAGATTATTCAGGCCAAT GTGTC[T/G]TTGGGCTGAGATTGATTATCAGCTGGGTAAGTTAACTGTTCTCTGTTTCA

NI-18063	105 GA ---	---	AGGCTTTAACTGATAACAATTTGCCCTTTAATCACATACAAAACTCTGCACCTTCATTCCTTCCTTC CCATGTTTTCTGATTTTGATGTAACCTTAAATTTG[G/A]CCTTTAACAATATACTGTAGCTGCA AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGCTAGCTGAACCTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAG[A/T]GTCCACTAGCCAAGTTGATCTCGAGTATCTACATGTGGT CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTTCATCCTTTGTTAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTT[C]GGGCCCTTTTATACTCTCCATATCTCAACTTGTAAAGC GCAATCTGTAACAGTTTTGGTAGTGGTATTACAGAGGAT[C]TTGTAATGGATTGGAGTACTTAC CACTAATTCATCTGCTCTGAAATAGTTCACTAACCAACTACTGACAAACAGTTTAAATTTGGTTCTT TTCAAGATAATTACAATTTGGAAGGGGACCAATAATTCACCTTTTAAATCGAAAAATATCTATATAC T/GICCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAAGAGGAAAA GCATAGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAAGTCCATGCTGGAGGTTAGTCTGGGG G/C]CGGGGGATGGACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG TCATCTGAACACTTGTGTAAGCCAGCATGGGGT[G/T]GGGAGGTTGATTATGGCTGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACCAAGTACAGTGGGCTTTCTGTTAAAAAGTCATCCAAA ACAGATGTCAGTTGTTGAATTTGGCCATTAAAGTATGGGGCTTTCTGTTAAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGTCTATACACGAGGACAGAAACATGA[G/A]CTGGGAGTAGGCTCT GACAGAGGGTGGGCTGTC GATTTGAAGGGATTGCTTTATTTAAAC[G/A]TGAAAAGCGTGATAGAGAACTGTTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAAGATTG TAGGAGGGAAGGAGGTGGGCTGCCTGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCTTACTTCCCCCATAGAT[C/T]CCTGACAATGTCTGCAGAAAGCCTCCAACTGGAAC TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTTT ATCTATTTGGTCTGAGAAATCCACAATTTTGA[G/A]GAAATCTTTTGCCAATTAATGACATATTCTG CAG TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTTT ATCTATTTGGTCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAATTAATGACATATTCTG CAG TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTTT ATCTATTTGGTCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAATTAATGACATATTCTG CAG TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGCCAATTTTTT T/GJATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAATCTTTTGCCAATTAATGACATATTCTG CAG
NI-18078	86 A T ---	---	
NI-18091	90 T C ---	---	
NI-18119	38 T C ---	---	
NI-18142	66 T G ---	---	
NI-18178	68 T C ---	---	
NI-18244	35 G T ---	---	
I-18245	115 GA ---	---	
-18261	26 GA ---	---	
18268	88 C T ---	---	
'8299f	107 CA ---	---	
9e	101 AG ---	---	
d	77 GA ---	---	
;	67 T G ---	---	

WI-18299b	52	G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAITTAACITG[A]/AJTTTGCCAAATTTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATTCITTTGCCAAATATTGACATATTCTGCAG
WI-18299a	48	C T ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAITTAACITG[A]/AJTTTGTTTGCCAAATTTTATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATTCITTTGCCAAATATTGACATATTCTGCAG
WI-18307	76	G A ---	---	TCAACTTGTAACCAAGTTTAGCAGCAAGAGGATACTTCTTTAGAGACTTTTCAGTGGACTTAAACTCAGTTTCCGCTG[A]/AJTGCTATGTAAAGCATCCACGATGGTTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T ---	---	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGTGGGTACTGATTTATC[C]/AJTAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C ---	---	ATGAAAGTCACTTCAATCATAAAGGGTCAAGAGAAAGAAATGTTTTTCAGAT[C]/CJTAAATCTATGAAAAAGGTGTATCTGCTTGAATTTAAGAAACAACACAAAGTCA
WI-18395	77	G C ---	---	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTTCTCGGAAAAATTTGAAGAATAAAATTTGATTATCAAG[G]/AJTGTCATGGTTTATACATATCTCCTCTCTCTTAATGCAAAAGCTATG
WI-18398	62	G T ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACACTCAAGGGTT[G]/AJGATAACATTTGCCAGTAAACCAATAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18396	21	C A ---	---	CTCGTTGGTATTCTCTCATCC[C]/AJTTCTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATTTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAACTTATCAACTTGTACAAAGTCAATGAAAA
WI-8409a	20	C A ---	---	AAGATGGGAAAGAGGAAATC[C]/AJTTTCTTACTAGAGATTTTTTTTCCCTTTAATCCTTTTCAAATTCAAAGGATCATCAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCCCAAGTGCTA
WI-18442	62	C T ---	---	AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGACAGAGAGGAAACAAAAATAAGTTTCTGG[C]/AJTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAAAGAAAAAAGGTTTATAGGTGGGAGAGAGGA
WI-18452	38	G A ---	---	TTGATGTTAATACGTGTCATTCTGGAGATCGGCTAAAT[G]/AJAAAGCATAGTTATTATTAGCTTTGGTATTTCTCGACAGATTTAAACAAGTAAGACATATATCAACCCCTCATATTTTCCAACCA
WI-18489	102	A C ---	---	ATATAAGCTGGAGACTGTGGAGGGTGAGAGGCGAGTGGGACTAGCTGTGTTGAAAGAGAGAAATGTAGCAGTAGTAAAGATGAAAGACTGCAAGGATTCAAAACA[A]/CJGGTTATGGCAATAGAGGTGAAAAAGAAAAGGCCATATAAA
WI-18489	93	A ---	---	CTGGTGGGAGGAAACAAAATTGTGGTATATTATACAAATGGAACCTTTCAGAAAATAAGAAGGAAACAACCTGAATCACACAACATGGACAAATCTCAAATCATATTGCTGATGGAAGAAACCATTCATAAGAATACACAGTACAT

ST5	93 A ---			CTGTGGGAGGAAACAAATTGGTATATTATACATAATGGAACCTCTTCAGAAATAAGAAGGAA CAACCACCTGAATCACACAAATGGACAAATCTCAAATCATTTATGCTGATGGAAGAAACCATTCATCA TAAGAATACACAGTACAT
ST6	48 C ---			TTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTCTTTCCCTTTTGCACAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
ST8	158 A ---			GGACAGGACCTCTATTCGCCCTGGTGACAGCGGCTGATGGACTGAGGCCCGCAGGGATCTGGGOC CTCTCTCAGGGGCTCTCCAGGACCCAGAGCTGTCCTGCTTTGAGTTCCCTAGAGCTGTGGGGCCA GATAGCTGTCCTGAGTTGCAAGCACGATGGAGATTTGGACACTGTGTGCTTTTGGTGGGT
WI-18740c	104 GT ---			TCCTCAATTGTTGGGATGATGAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAAATCTCAATTTACCATCATGTATCCAGTAGTG[G/TAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96 CG ---			TCCTCAATTGTTGGGATGATGAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAAATCTCAATTTACCATCATGTATC[C/G]AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105 CT ---			CCAAAGTCTCTGTTGCTCATAAAGAAAGTTTGGGATGGGAGAGAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCATTTTACAGAGGTAGCACA[C/TT]GATTCACACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCTCAGAACCATTTGTGTGTTCTCTT TGAAGCAATGACAAAGCACITTTACTTTACGGTGGTTTTGTTTTTCTTAT
WI-18746	114 GA ---			GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTTATATTACTTTTGTAATATCTT[G/ATCCACATCTACTTCAGCT TTGGATGGTTACCG
WI-19112i	212 GA ---			CCGTGTTACACACACACAATGGCAAGCATAGTCGCCCTGGTTACGGCCAGGGGGAATATGCCAAGG GACCCCTTAATGGAACACACAGATCAGTAGTGTCTATCTCATGACAAACCACAAAGAACCGACGACAAA TCTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTTAAAGAACACGGTGATATCTTTGAG GGTGACAAGGC[G/AT]CTCTTCAACACAGTTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC ---			TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTCTATCTTGAATGCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAAATTTT[C/A]ATGATTAGCCGTGTAACCT
WI-19057i	175 GA ---			CCCAATTTATTAGCCAGTGTCTCAAAGAGTAGAGGCGTCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGGACTTTACCGTGACAGCGGAAGTGGTATTGTACGTCAGGACCGCAGCCACTG TCTTCATGCAGGAACACAGTGCCAGATCCCCACAGCTC[G/AT]CTCTTCATCTGGTTTGGCACA

WI-20103	168	CT ---				TGGGACTTCCAACCTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGCT AGGATGGACAGGCTGTGGATATGGAGTCAATGGTCAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCCA/C/TTCATTCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	GA ---				GCCTACCCATTTGCACATATACATATGCACCCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA/GA/TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACCTACCCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAAATCTCAAGACTGGCTCATGGCAAAATGAATAIGCTAAATTTGGGG
WI-19911b	116	AG ---				TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCCTCTTTTGAAAGAACGT TTTAGTCTTTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTTTTA/GIACACTGTTTTGAAA ACTTAAAAAGTGCAGCAATA
WI-20613c	165	AG ---				GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGA/GA/GIAAGGGAGTTTCCACGCGAGCCAGTGGTGAGC TGC
WI-20613b	156	AC ---				GTCCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAA/CIAGTTGGAAAAAAGGGAGTTTCCACGCGAGCCAGTGGTGAGC TGC
WI-19984	47	AG ---				CAGTAAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA/GI/TATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAATGAAGGCAGTTTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	TC ---				GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCTATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTGTGGGGACTTACACATTCAGTTTGACAGI T/CITGAAAACCAACTGGAGCTGCTTTTCCAAAGAAATGTTCTGTTGTCTTCAAATAGGAATTCATG TTATTCTTCTTGCCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49	GA ---				GAGTGCCATACCTTCTCCAGGCCCTCTGCCCAAGAGCAGGAGTGCCTG/GA/AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACTCCCATCCCGTAAGACCTCTCTTCCCTTCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	GA ---				AGCAGTGGCCTTATTGCATCCCAACACCGCCTCTTGACAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTACAGTCTTTTAAAGTAAATGGTCGAGAAAAGAGGCACC/GA/GGAAAGCCG TCCTGGCGCCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGAAGATCTCAAAGGAGCGAGCAT GTCGTGGACACACACAGACTATTTTAGATTTCTTTTGCCCTTTTGCAACC

WI-20146	31 T C ---	---	---	TGAGTCTTCTGTAAATCATTGAGCAGTTAGCT/CJCAATTTGAGATAAAAGTCAAAATGCCAAACACTAG CTCTGTATTAAATCCCATCACTACTGGTAAGCCTCATTTGAATGTGTGAATTCATTAATACAGGC
WI-18922	74 G A ---	---	---	TAGGAATTGGTTACGCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC/GAJTCTGGCTCTAATTCACAGTGCTCTTTCTCCTCACTGTATCCAGTTCCCTCCACAGAG GAGCCACCAAGTTCTC
WI-18763b	53 A G ---	---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/GJATATTTAGAATG TACCATATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTGTTTTGCCAA
WI-18763a	38 A G ---	---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/GJTGACGATGATGTGAATATTTAGAATG TACCATATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGGTTGATGAACGTCA TGTGTTTTGCCAA
WI-18771b	75 G A ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAGAAGATGTTGGG AACAGAA/GAJAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCCTAG/GJAGATGTT GGGAACAGAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---	---	---	GGGAAAAATTTGAGACGCAATACCAATAGTTAGGATTTGGTCTTGGTGTGTTGATGAATCTGAG GCC/T/CJTGATTAAATCTTTCATTGATTGTGATTTCCTTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51 C T ---	---	---	ACAAAGTCCTGTAGCCCCCTACCTTTCTGTTTTCACCTTTGCCAATGA/CJATCGGGTTGGTTT TCCTGTATTATTAAACGGTTGGTTTCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---	---	---	GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTGAACCTTCCCTTTCCCTGCTTCTCTCCTCATCA TCATTTCCCAACAACATCCTCTGCCA/CJ/JACACAACAACAAACGTAAAGTTTCATTTGGGCCAAAAATTGA GC
WI-19970b	167 G A ---	---	---	TATAAGCCCGAGTACCAAGGACGGCTGTCTGGCCACAGACAGGGGTGCCTGTGGAGCCTGCCACCC GGCCCCGGCAGTGCAGTCAGTCAGCGGGGAGGAGGTGCCCTTCTGCCAGTTCCCTCACTGGGGGAOC AGCAAAGGCCTTCTCACTGGTTGGTCAAAG/GAJTAGTCACCTTGGCCTGGTGATCCACAGAGGA TGTTGTTCAAAACCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA
WI-19970a	126 T C ---	---	---	TATAAGCCCGAGTACCAAGGACGGCTGTCTGGCCACAGACAGGGGTGCCTGTGGAGCCTGCCACCC GGCCCCGGCAGTGCAGTCAGTCAGCGGGGAGGAGGTGCCCTTCTGCCAGTTCCCTCACTT/CJCGGGG ACCAGCAAGGCCTTCTCACTGGTTGGTCAAAGGTAGTCACCTTGGCCTGGTGATCCACAGAGGAT GTTGTTCAAAACCAGAAATCTTTAAACGACTGACCTTCCCTTAAAAACAGA

NI-19067d	202 T G ---	---	TATTGCTGCTTGTCACCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTAGGCTCTGGAGAATGTTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAAAT/ GACATAGTATTCCTCTCTCAAGACGTGGGGGAAATATCTCATTATC
NI-19067c	153 G C ---	---	TATTGCTGCTTGTCACCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGTCCTG[C]GAGAAATGTTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTATC
NI-19067b	151 T C ---	---	TATTGCTGCTTGTCACCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGTCCT[C]GGAGAAATGTTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTATC
NI-19067a	57 C G ---	---	TATTGCTGCTTGTCACCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC[C]GCTGGCTG TGCACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTT CTCTGGGCTCTAGGTCCTGGAGAAATGTTGAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTATC
NI-19106	247 T C ---	---	CAAGGCAAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTTACCTAGCATTTCAAACCC AAATGGCTAGAAC[A]GTTGTTTAAATTAATTTTCAAAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCTGGTTCAATTTCTTTCTTTTAAATAAATTTAAGTTTT
NI-18944	147 A G ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGATTGTTCATAATACATAAA GTTCTCTGTAATTACAACTAAATATTATGCCCTCTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTTGCTTTTTTAGATTTATTGTCCTCATGTTGAGTTTAAATGCCACAAGACATAATTTA AAATAAATAAATTTGGGAAAGGTGA[A]ACAGTAGCCCCCATCACAT
WI-18952	232 G A ---	---	CACACCTCATGTAGCCTCACGAACTGGAATAAGCCCTTCGAAAAGAAATGTCCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTGTTGCTGATTTTGACCTTGATTTCAAGTTAACTGTTCCC CTTGGATTGTTTAAATACCTGTACATATCTTTGAGTTCA[A]CTTTTAGTACGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGACGTGCTTGGAAGACAAGTCTGTGGCTTG
WI-18932d	177 C T ---	---	

NI-19042	193 A C ---	---	---	TTTGTGAGTGTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAAGGTGAACCTTTGTGCTTCAAGACATTGGTGAGAGTCCAACAG ACACAAATTTATACTCGGACAGAACTTCAGCAATTTGTAATATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGTATTAACTATCTCTTTGGACTTCTGAAGAGACCCTCAAT
NI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGCCTTATTATAAATTCATTAAAAACACTACAGGTGTGAATGGTTAAAA TGAGGCCCTCCAGTTTCAATTTTCAGTTATTTCTGAGTGTGCAGACAGCTATTTCGCACTGTATTAAAT GTAACCTTATTATAATGAATAATCAGAACGAGTAGACAGATGTTGGTCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
NI-18851	90 T A ---	---	---	GCTTCAATTGGCGATTGATTGAGTGCCTCCACAAATGTAACAGGGTTGGTAGTTACTCATTTTGAAT ATACCTTTTCCCTTATTGTAATCTT[A/G]ATAATAGGATCCTGGAAATGAGACCTGGTGGAA
NI-18821b	76 T C ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
NI-18821a	69 C T ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGGAACTTGCCAACTTCGTGTGTCAG GTGCTGTGT
NI-19021a	20 C G ---	---	---	ACTCCTCTGCTGCTGTCCAT[C/G]ACTGTCTCTTTGAACCAGGAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAGTGTCTCTCCATCACGTTG CTACCTTACCACACTTCCCTCTGATTTGCGTGAGGACGTGGCATCTACTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTCTGTC
NI-18908	70 G C ---	---	---	TGGAATTTCCCTTTCATCTGGAACCATCAGAAACACCTCACACTGGACTTGCAAAAAGGGTCAGTA TGG[C/C]TAGGGAAACATTCATCCTTGAGTCAAAAAATCTCAATCTTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
NI-19037b	155 A G ---	---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGTCCTAGCCACGCCCTGTATGACCCGCGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGTC CCCTCCCTTACGAACAC[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTGCGAGGGACCA GTGCCAGGCACTGGGGGTGGAAAGTGTGGTGACACAGTGAATGGGAGTGG
NI-19037a	47 C A ---	---	---	CACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGTCCTAGCCACG[C/A]CCTGTATGACCCGCGCAA ATATCCCCAAAGCTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCATTTCTGGAGAGGG GTCCCTCCCTTACGAACACAAACCCAGCCACATGACTAGCACGCTGAGCTGCGAGGGACCA GTGCCAGGCACTGGGGGTGGAAAGTGTGGTGACACAGTGAATGGGAGTGG
NI-19064	66 T C ---	---	---	TTGAGGAGGTGGGTGAAGTCTCTCTGGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTCTCT/ C/GGGCTCTTCTGGACCTTGACCGTGGATACAGGCCCATGTGCCATGTTGGGTCTTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---			AGCCTGTGGCTTATGTACCCAAACAGAGGGGTCTGAGAAAGTCTGGCTGCCCTGGGATGCCCCCTGCC CCCTCCTGGAAGGCTCTGCAGAGATGACTGGCTGGGGAAGCAG/GTGTCTGCTGGCCATGGAGCC TCATTGCAAGTTGTCTTGAACACCTGAGGCCCTCTGTGGCCACGAGGCACACTACGGCTTCCTCTCC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTTGGCCA
WI-19016b	184 C A ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCATCTCAA/C/A/CTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---			GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTAAATATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGATTAACGAAGTTCAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAC/C/TTGTATACAGAGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTGTCTGTGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGCAATTTATTTCT/C/GATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCC ACCTCACTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGGTAACCTCAAGCCATG AGTAAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAGCAACTCAGTGTGCCC CTTAGGGTGGGAGCTCTCCG/C/A/CTACCACCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAAT/AJATAAGGTAACCTCAAGC CATGAGTATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAGCAACTCAGTGTGT GCCCCTAGGGTGGGAGCTCTCCCCCTACCCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTCTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---			TCCTCCAGCTCTGTCATCCTTGTCTTGGGGTCTGTGTTACGGCCCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGCCCAAGCTCTCTAGAGGCTCCA/G/ATCAGAA CTGACCCCTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCCTCCCCGGGG
WI-20860	224 G A ---			CTCTCCCTAAGGAGCCTTGGCCTTGCAGCCCCCATTCAGCAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGTCTCCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGTGGCAGACCCAGCCTTGAGAGCTCTGTAGAAC GGAAGGAAGGGCGGTCTT/GA/GGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---			GACGTGGACAAAGGAGGTTTAAATGAATACCTTGTGTTTGT/C/CTATGTTCAAAAAAGAGTATTAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGCCACCCACTCTCGGGCATGCTGCAATATCTCTGGGCTCAAGTGGGAGGCCACGTG GGAACAAGGCCTCAGAAACAAGGACATGCAGCCTCCCTGAGCCAGTTCTT

WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTC/A/G/GACAAACAGAAAGGACACCAAGCCTGAAACCCCTCGGACAAACAGCAGAGTTACAGCTGAGGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCACCCCTCC/TCC/TACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCT/G/ATGCAGCAGCATCCTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAAACCCCTCGGACAAACAGCAGAGTTACAGCTGAGGGATGTCCTGGAGGTTCTGACCCATGAGAGGCCCCCTCACCTCCTTCACCCCTCCTACCACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTGGCTTTGCAATTTGCGATTTGGAAAAACCACCTTGGAGAAGGGACTTTCTCTGCAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/G/AAAGCTTAGAAAGGAAGTAAATGCTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGGGCTCACGCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTGGCTTTGCAATTTGCGATTTGGAAAAACCACCTTGGAGAAGGGACTTT/GTCTCTGCAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGCTTAGAAAGGAAGTAAATGCTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGGGCTCACGCCTTATTAATCCAGGCACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATTTCCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCCATAACCCCTTCTACATTGGAAAGAGCACACCTTGATACAGATGGCTCCGCGTGAAGTCTTTTAAACGGACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACACGTAAACCAACACCTCTTTTCAGAACAGAGAGCGTTAAAGTAAAGGGCA/C/G/TTCCAAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAATTTCCATGGTCTTAATTGAACGTGATGTTACTTTCTTTTGAATATCCTTTTTTTCATTAAAAATAATTT/C/TCTAAACCACTCTATGTGTTCAACCTTCTGTTTAAACATAAGATATGGGTTTTGGAAAGGCCACAGTCACCAAGTCCATGAAGTGGCGAATGGTCCCTGTTTGGAAAGCTCTCAGGGTGTCTCTCCAGAAA
WI-19909a	29 T C ---	---	CCAGAAATAAAGCCTGAATATTCTCTTTCT/C/TTAAAAATAAATTTTCTCTCTTCTCTCCAAATAATCTTAAATGAACCTGTTCTAGTCTATTTTAAATCTAGGCAATTATAACACTACCTAGGCGGGTTTTTCTCTTATACCTTGTCTGTACTGTGGAACTCACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTGTCTAGGGGCATGAGACATTAGGAAGGCCACAATTATGAGTAATGAAATGTGGAGGCTGATGAGAAGCTACTGCTCCATTGTTTAGCAGGAGGCAGGAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATAATTTGGGTGACGTCATGCATCCCCCATGCATTGGTTT/G/C/ATGTCTCCAGTGAGCTGTGGGCAAGTCT

WI-20113	60	T C ---	---	TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGAACCTGAAATACTGT[C]GGA AACAGTAAAGCAAATTAACACACAATAGGAGGAATTAATTTCAACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATCAGCAATAAATCTATTCATAAACCCAGGTAGATAAATGTCCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCAATGGATTCCGTAAT
WI-20895	107	G C ---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGACGGTGTGGC CACTCCCAAGGAGCAACACTTGACTTCATTAAGGCAAA[G/C]CTTACTCTGTTACTTTTCCCTC CCACATAGTTTAACCAATAAGAAAGGCATTCATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C ---	---	CCTGCAATCACAAAAGTGAAGTGAATTTTGAATCATACTTGATTTAACCCACCTTCAGAAA TTCTA[T/C]AACAACACTAGCAACTTCCCTTTATCAGA
WI-19415c	161	A G ---	---	CTGGATTTTAATAATTTCTGGCCTAATAACCAAAATGTAATCAATAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGGCAAGATCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT[G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCIG
WI-19348c	103	C T ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCGGTGA[C/T]GTCCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAACCTGCTCTGCTGTGTAGAAAGCTTCTCC
WI-19348b	98	G A ---	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCTTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAACCTGCTCTGCTGTGTAGAAAGCTTCTCC
WI-19635	98	A T ---	---	ATTAGTTCGTGGGCCACATTCAAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAAAATACAGTATTAT[AT/TA]TCTTATTGTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTCTGAAAGAACTTTGCCTT T
WI-19641a	46	A G ---	---	TCCAAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCAGTAG[AT/G]TATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGTTATTTACAGAAGATGTGAGGCTATCTCATTG AGTTATTAAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A ---	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT[C/A]GGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTAATTTTGTATGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T ---	---	TCTGCCATGATCACATTGTGATGAAGAACAATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCGCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGCATCACCAGCTGTAATCTAATAGT GAAAAGGCCAAATGATGCTCAGTATCATCTGCTGAAAAACATTTTTC[C/T]CTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTTCAAGGTCCACACGTCAAAAAACAACAGCC

WI-19673a	35	G A ---	---	TCTGCCATGATCACATTGTGATGAAGAACAATGATG[A]TCACTAGTAGGTAACCTTCTGTGTCATTG CCTTACTCTCAGTGAGTGCTAGTGGATTTACCTACCCCTGCTTTTGCATCACCACCTGTAATCTAAT AGTGAAGAGGCAAAATGATGCTCAGTATCACTGTGAACAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAAGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAACACAGCCC
WI-19724	35	A G ---	---	TTTATTTGGGAACAAGGATTGTAATTTGGGTA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCT
WI-19307	196	T C ---	---	TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCCAACAAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTGCCCTCATGAGAAATGGTGGCTTGGGATGGAGGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAAAGGAAACCAAGCAATGATTCCATAGAGGCCTTTAAAGAGAGACCCG[T]CJTG AAATGGGCCATGGTCTAATTTGGTGTGAAATAAATAACCTCTTTGGCTG
WI-19269	85	A T ---	---	CTTCCCTCATCCCTCTCCACCACACCATCCCGGAACAAGTGCTCCAGGATCCCTGCCACTGGC CATTTGGAGTGTGTC[A]TJTTGGGTAGCAATGTGGAACCAACCAGGCCCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTGAGGGCTTTGCCACTTGTCTCATAGCGGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCGAATCTTCCCGGGCGTAGGCA
WI-19946	122	C T ---	---	CAATGGACTGAATGAGTGGTGGTGGTGGGGCCACACACCTTCAATACACGTCAGGTG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGGT[C]TJCTTCTCTG ACCCAGCGCACTCAGAGCCAGGTCTGTTTTCAAAAACGCAITTAACCTGCCCGCAGAGATTCA CGTAGGCATCTTAATAAATACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---	---	CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACCTTACAGCACACATTTTTAGGGCCAAAGTTTGGATCTGTCTGGACCT CAATG[A]CTCTCGGAGAGCAGCCAGTTCAGCAGCAGATACCTTACAGCTTGTCTACTCTCAA GTGATGGCCACAGAGCTTCTGAACCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---	TTGGTTGGATACCTTGTCTGGAAGAAAAAGCAGTTTTAAT[G/A]GTATTCAAAATACCTTTTAAAA GTATCTAGCACAAAGATTTCTGTAACTAGATTATGTTGTAACCTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATCTTCCAAATCTATCTTGGCTCTCTGAAAAAAGTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATATGGGATTCTTTTATCTT
WI-20218	26	T C ---	---	CCACACACTCTGGTTTTATAAGCTAT[C]AGGACAGAGCAGAGATGGAACCTGAAAAACAGGGTAG AAAAAACATAAATTGGAGGGGAACAGTGGGATGCAGAAAAGATGACAAACAGCCACATGTGCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAA
WI-20295g	154	T G ---	---	CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTAATATCTCCAGGCTTATTGGGAGGGGCTGGCTCTACCCCTTTCTTTTCCA TCCAGTCTATTGCCAGAT[G]CCAGAGAAAGCGGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTGGCTTCACTCTGTGACTCTCTCATGCTGGGACTTGCTTTGGGG

WI-20361a	192 G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGGCTTATGCAAGATGACAGAATATGTGAAATCTGATTTGCCAGAGTTACACTCTGCACCTCCAAAGCTACAACAGTGCCACAGCTGAGAGGTTCCCTATCTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC
WI-20572	75 A G ---	---	AAATGGGAAATTCCTAACTACACGAGACAATGGGTCTACAGTAGGCCCGGAGCCAAACCCAAACAAATAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCTTCAGAAATT[G/J]CATAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTGTTCAAAATTCATCTTTCTCAAATTTTAAATTTGTTTAAATCCCAAAGGTGCTTATTGAATCTTCAAAAATAAACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 G A ---	---	CATGACAAAAGACAAAGATCAAGGAGTAACATAAATTAAGTTGAATAAATAGTATACAGCAATCTTCACTTTTTAAGAAATGTGAGATCCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAC[G/A]GGAGCCGAGCTCTCCGCATTCAGG
WI-20593	79 A G ---	---	TGACCTCATACTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTGCTGTACTTCAG[G/J]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACAGATGAGGAAGAAAAGCTGTTAAAGGAACCTCAGGATGTTGTAGGAAGGGGAGTGATGCCAGGCCTTCACCAGACTATCCAGAAGCCATTCCATGGGGTATTTGGTCTGCATCTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCAT/CJATGTATCTGTCCCTGTGCTTTTAGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTCTTTTCCCTCGTGGTATCAGTGAAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAAATGGCCATGGAACTGAGC
WI-19066f	239 A G ---	---	AAAAGGCCACGTGGGATAAAATCACTCACCATCGACGCCACCATTTTGACAAAGGGAGAGAGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACITTAAGCTTCAGTGAGCCACAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGATGCTCAATTACAGTACCTTGCAAGGCAAACTTTTCTTAAACGCCCTTCACT[G/G]GTTTCTTTTAA
WI-19066g	184 C T ---	---	TGACAAAGGGAGAGAGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACITTAAGCTTCAGTGAGCCACAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTACTTCTCCATATTC[G/J]GGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA
WI-19066f	148 T C ---	---	TGACAAAGGGAGAGAGGGAAATTTCTACTCATTTGCAAGGAAATCCTCACITTAAGCTTCAGTGAGCCACAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGGCATATGTTCTTGCGT[G/C]JGGTCACCCCTGTAGCTGAATTACTTCTCCATATTCGGATGCTCAATTACAGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTAA

NI-19066e	147	G C ---	---	TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACCTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAGCTGG CATATGTTCTTG[C/G]TTGGTCACCCGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTTA
NI-19066c	100	G A ---	---	TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCACCTTAAACCCCATGAACCTTCAGCTGATC[G/A]TCCCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTTA
WI-19066b	87	C T ---	---	TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TTAAACCCCATGAAC[C/T]CTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTTA
WI-19066a	72	C T ---	---	TGACAAGGGAGAGAGGAAATCTACTCATTGCAAGGAAATCCTCAGTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGGCATAATGTTCTTGCGTTGGTCACCCGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTTA
WI-20660	105	G C ---	---	TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTG[C/G]TTAATAAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATTCATCTGTTTCTGTACAAGATAGAACA AAGCTATCCACCGCGCCCCCAAAATACGTGTTTAAACAACACTATGTTTTAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGCGGTCTCTTGGCAGGCTCCCTCAGTCTTCC TCCACCGCGCTCTTCTTCCAGCGCTGCGCTGCATGCATGTGCACCCCTTGG[C/T]TCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120	C T ---	---	TTCCCCAGGGTCTGTATTGCAGCTAAGCTCAAATG[T/G]TATTAACTTCTAGTTGCTCTTGTGTTG GTCTTCTTCCCAATGATGCTTACTACAGAAAGCAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACCGGCAACCTGTAAGTCCCTTTTAAATGGCATGACAAGGTGTGC AGTGCCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49	A T ---	---	GAAAGCCAGAGATTAGCCCCGCAATCCGCACTGTCAACCAGGACAGAA[T/G]CATGGACAAGGGA TGAGCTTTACAAAGATGATGCACTTTGGAGATCAGAAAAATCATATTTAAGCAAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35	G A ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC[G/A]GTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGCCCCCGTGGATCCTGGTCTTAGGCTGGACACAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTGCAGACGCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA

WI-18919	26	CT	---			TGGATGAAACCACAGGGATTCCGGAC[CTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] TTGTTTGTGTTGTTGTTTATTTTATCTTTGGCCATACCACAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64	GA	---			CTTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATATATGCAAGTTAAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38	GC	---			CTTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23	TG	---			CTTTCTGGTCAAGGCTTTGGACAT[GTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATATGCAAGTTAAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170	GA	---			TCAGAAGCAGACATGGCATCTGTTCCCTTGGCTTGGTTGGTTGTGTACCTTTTACGAGACCTGAATT TTAGAATTGCCAGTGTCTGCCAGAGTGAGTGAGTAAATCTCCCTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCAATAAACATATCAACCA[G/A]TAGCAATTAACCCATTTTATTCCTGTCTT AGTGTCTGAAGATGCTCACCAGTTTCTGTGATACAGTAAGGCAGCATGCT
WI-19212	46	TA	---			CCAAGTTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT[A]GTTTTCAGAACCCAAATGT CCTCAGGTAGTTGGAGCATCTCTATGAGATGGGATATGCAGATGGCCTATGGAATGCAAGCTGC ATAATTAAACATTTATCAAGTCTCTTACAATTTATTTCCGCAGCATGTCAGCTAAGTAGACCCA ATGGGAGAGAAATGCCGTCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210	GC	---			CTGTTGAAGGCTTCTCAGGCAACTCCAGCTTAAAGCCCTAGACAGGTAAGACACACATTTGGATG GCAGCATGGGTTTCTCCCATTTATGGCATGAAATATGTGTTTAGAATAAGGAACAAGCATTAAT CCTTTGCCAACAGCCTCACTTAAGAGGCTTTTGTGCTAGTCAAGCAACACTTGCTGCTGCTGCCC CTTGGAG[G/C]TGCAITTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214	TC	---			TTGAAATCCCAGTCTCTGGCCCCCAGGCGGTCTGTCAACATAGATGTCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTCTTGATTTCTGAACTGGAACTGAACCAAGTTTGCCTTTCTCCTAGTCACC AAGCATACTT[C]TCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198	TC	---			GTCTCCCCAGAGTCTCTGCACCCCCAGCCCTGTCTGCTGTAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGGCTTAGTTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACCAGGGGGCCATCTTCTCAATACAGCC[T/C]G CCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGCTTGGCTGTCTGT
WI-19135	20	GA	---			CAGTTACCCCTGCTTTGCCCT[G/A]AAAGTGTGTCATCAATTTGTAATTTTAGTATTAACTCTGTAAAAGT GTCTGAGGTACGTTTATATATAAGGACAGACCAAAATCAACCTATCAAGCTTCAAAAAC TTGGAAAGGGTGGATTAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54	G A ---	---	TACACAGAGGGTCCGACCTGGACTCTGAGGGTGGGTGTGGAAGGGGAAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTACCCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGTACACTCTCTGGCTATCTCAGGGGGAATGGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTCCAGAAAGCAAGGACTGCCCTTCATTCAGCCTTGCTGACCTCCACAGCCTTCTTAAGG CTCAGCCCCACGGGACTCTGTGGCTGCCAGCTTGTGAGCTATCTATATTCATTTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAACCCCTCTCTCCCTGGT CTGGCTCTGCTGGAGCG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGAGTGGTTGGCAGACACACACTAG[C/A]ATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTGTCTCTCTTGG GGGCCGCGAGATCTAGCATCTCTGAATCCTGGCTGTCGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA C/TJGGCAGATGCCTGACAGAGAGTGGTTGGCAGACACACACTAGCATTTTACGGGTGTGGGCAC ATGGGTGTGGCACCTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTGTCTCTCTTGG GGGCCGCGAGATCTAGCATCTCTGAATCCTGGCTGTCGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGTGATGATCACTGTGCTGT[G/C]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCGTGTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGCTCTGTAGCTTCTCTTCACTGCCCCAGTATGCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGA[A/G]GCTTCATGTAATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCGACGACCTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCCAGTTTAGTTGGGATGATTTGATTTCTGTGTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCTAAAGGACTCTGCGGAAC[C/T]TTCACACCTCTTCTCAGGGAC GGGCAGGTGTGTGTGGTACACTGACGTGTCCAGAAGCAGCACCTT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGAGAAAGAAATGCACTAAGACAAGAACATTTCTCTCATAGAACATTG ATCTGTTTTACAGGAACAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A/GJTAGCTATTTTTTCCTAAGACATTTTCATTCATGAATATTTCAAGTTTTTCATACTGTACA CATTTCTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTG

WI-19134c	263 C T ---	---	CTCCTGTTCTGACAGGGTGACACAGCCCTTTTCACACTCTGCTCCTCTATCTTCTCCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGGGGTGAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACACTATCCTTTTCAGAGCAC TTCAATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGGAAAGGG
WI-19134a	162 T C ---	---	CTCCTGTTCTGACAGGGTGACACAGCCCTTTTCACACTCTGCTCCTCTATCTTCTCCTGGGTAGA TGCCCTGGGTAGGGCTGAGTACTGAATGGTCTTCCATCCCAAGGGGTGAGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACACTATCCTTTTCAGAG CACTTCATCCACTTGTCTCCTCCTACCTCGGCACCCCTGGGTGGGAA
WI-19224	112 C T ---	---	GGTTTCACCAAGTCTTCCCAAGGAACTCCGATGAAGTGTCCCAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAAACAGAGGAGATAATCTC/TTCAGGATGCCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTCAATAATCCAGCAGGCCAGAAAGACTTCC AGGAAACTCATTCAAGGAGGTGAAATGATGATGACTCCTCCAAGATGAAAA
WI-19201	179 T C ---	---	GCAGCTCCTAAGGACCACCTGGCCATTAGCTCTTGTCTTTGATGGCATTCTCTTCCACCTTGTCTTCTC CTTTGCTCCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCCTCACACTGCC CTTCCGCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACT/CJTGGGGGATAAAATTCAAAAA GTGTGATGTGTGCTCAGAAAGTCAAGTCCATGCTGTGCTTGGCCTCAA
WI-19034	45 T C ---	---	GAAATGGCTCCACTCAGAGCTACCCGGTGTAGGATAGGGGAAT/CJACTTCTATTACATTAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGCATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTTCTGTGCGAATTGAC ATTTGCTACTTATAAACCTAGTCCCTAAGTCTTCTTATGCTGTGCTATAATA
WI-19102	25 C G ---	---	TGTTCTGAGTCACGCTGAGGAGAG/C/GTTCACCTCAGGAGTTCATGCTGAGATGATGATGATTCA TGCGACGTATATTTCTTTGGAAACAGAATGAAGCAGAGGAAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGAGTCTAGAACTCCTGTAAAGTTTGAACCTCAAGGGAGAAAGTAT AGTGAATGAGTGTGAGCATCGGGCTTTCAGTCCCATAGAACAGAAATGGG
WI-18548b	65 A G ---	---	AAAGGAGGGAGAATCTTTTACATAAATGCCTTGATCATCTCCAGTCCCTCCTCACTGGGGAA/A/ G/AAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18548a	62 G A ---	---	AAAGGAGGGAGAATCTTTTACATAAATGCCTTGATCATCTCCAGTCCCTCCTCACTGGGG[G/A/A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97 T C ---	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT/C/AAGATCCACAATTGCAAAGGCCACTGCTGGCTCA CTTCCCTCACA
WI-18501	121 C T ---	---	CAGAGGGAAAAGTTTATTGATCAGCCACAGAGGAAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTGGCAGGACAGAGGGGCG[C/T]GGACAGCA GCGCATGCCACAACATTCA

WI-18017	87 C A ---	---	ACAAAGAAAATGGAAATAGGTTGCGAAAACCTTATCTGCGATGTACAAAGTAATCCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTCAATAAAATTATATCTCTTTGCAT CAGAGCTGGTGGAATCAT
WI-18148b	101 A G ---	---	TTATTGCGTTCTTCGATAACCTCTCTTTGGGACTATGAGATCATCAACAGATGTGAAAACGAAAGCA GTGATTTAGAAACGNTCGATTCTGAATATCCC[A/G]TGGCGCATATGCAAAAGGAAGATGA
WI-18254	64 T C ---	---	TATACGGATCATGTATTGTGTGACCAACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCAC[T/C]]GCCAAAATCCCCTCTGCTTCTGTTAGTCAAGTCTCTCCCAACCCAGGACTTGGCAACCTGTTT TCGGTCTCTAGACATTT
WI-18265b	117 C A ---	---	CAAATGGGTGGACTGAGTGATAAAACGCTATTGAGAAACAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACGGCTG[C/A]GTCTTCAACCTTTTC CTTGGGIGGTTCTTCAG
WI-18295	40 C T ---	---	ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAGGTTGATTACT TCCTCTCCAAGGATGATGTTTAATGAATCCCCTTNCCTTAGCTTCATTCTTCATAATGCCAAA
WI-18459b	64 T C ---	---	GGGCAAGAGACAGAGATTTAATTGAATAAAACCTCCAGGCTGTGACACGGTGGGAGACACAAAT/ C]GAGTAATTAAACAACATAATATTANATGACAGTGAATTAATTAACGTCCTGGTAAGCCAGAG GGGAGGAGGGGCTTTCA
WI-22585	56 A G ---	---	TTTATTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGCGAGGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---	---	GGGCTGTGAGTAACAGAACTTGATGGAAAATGGC[A/G]TCTGTGTAGATGATCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---	---	GCCTTTGCTCTTTGCTGCTCAGAGGCCTCAGATGGATACGCAACTTCCTTTTGAACCTTTTAT TTTCCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGAGGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T ---	---	GGCAGGATCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAGATATTAATGCCACT GAAGTGTTCATTTAAATGGTAATTTTCATGTTATGTGTATTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAAATTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---	---	TGAGACCATCCTCCTCAACAAAGAATCAGTCAGTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---	---	TCAGAAATTGCTTCCACTGCCCCAAACCAAGAAATTTAATGAATGNCNTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCCTGGAGGTGCATGACAGGATTAGTCTCTGT[T/C]CTTGGT GCAAGTTTGAACCAAGTATTATGTACCATTCATCAGAGCATCTGTTTCCCTGTGAGATCCCCACTAG

WI-20561b	94 T C ---			CGTTGCTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTCATTATTG TACTTCAGATGAAAAATCCTTACATGTC/CJGGAATCAATGTCTTTTAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20561a	25 A G ---			CGTTGCTATTTAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTCATTAT TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI-20116e	69 T A ---			GCTTTCATTTTCTGTCACCCACCCCTGCCACGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT A/T[A]ATAAATCTATATCATATATTTATACACACAAACACATTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATNGGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20116c	59 T A ---			GCTTTCATTTTCTGTCACCCACCCCTGCCACGTTATGTTGGCCTTCAATATATGGCGT[A]TAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATNGGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20116a	22 C G ---			GCTTTCATTTTCTGTCACCCAC[C/G]CTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAAATCTATATCATATATTTATACACACAAACACATTTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGGCCTCTCCCATGCCACTTAAAAATNGGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCCGAGATAA
WI-20466b	133 G A ---			AAAGATTTGCAGTCTGGGACACAGTTTGGAAACACTATTTATAAGGTTGCACATATTACAAACAG NTCCAAATGGTGAAACIGGTATTTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC[G/A]GTGAACATAATGTTTAAAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---			CTGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACATAATCTTTGTATTTTTCGAGGAAGAAGATCT ATAAGATTGACTTACTCATTTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI-21034b	148 T C ---			AGAATGGACAAATGATGCAGATGATTTGTGAGCATTTTGTAGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACAIGCTTAICTAGCTAACCTAATCTGTTTCTGTAGAATTAAGTGTATGG GAGATTGGATAGAT/CJGCTAACCTATCTCAATTTTAAAGTAAATGTGAGCAA
WI-22091c	205 G A ---			GGCGTGTATTTGATGCAATGTCCCAACCAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTACCTCCCCCTTAAGTGACTCATAATTC ATTACTTGTGCTGTAGCTTTTAAAGGTTTAAAAATGTGTAGCATTAAGTGGTATTACTTGAGGGCA ACA[G/A]AATTACGGCTTAACAACACACTAAATCATGAGGCTCAGGGATTG

805a	45 A T ---			CAACTGCTCTGAGGCTCTTCACTAGCTGATTATAATCCTATATTATJAAAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTTCTCAAGGTGGATATGTTGGTAATGCAGATCCATCAATATGIGGTT TTGTTTGCTTTTGTAGCTTAAGTCTGTTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
778b	155 T C ---			AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACTTTTTTATTGAATTATTGAC TCTGCCCGGTGTCGTGCTTCACTCCAGTCTGTAATGCCCTGTGTAGGTGGGTCCCCAG GTCTGGCTTCTGAGGTCTCJGGTAGAAGGAGGGCAGGTGGT
1-20907	241 A C ---			TGAGTCAGTGGTCAGATGGGCGAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAACACTGTCCTCT CAAATGATCTAGAGCTCATCTTGGCGTACATGAGGGCAGTTGTTGTTCTAGTACCCATTTAGCCC ATGGCTCTCAAGCCCAATTCACACTGGGGAACACACCCCTCACAAGATGCCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTTAJ/CJAATTATCTA
449b	222 C T ---			AACAGCAGCAGTCACCTCCAAAATGCAAAAAAATTAACAATTTTAGAATAAAATATAATGTTTA TAATCGGGTCAAGAAANTTGAAGGTACAACAGAATCAATCAACGCAGCACTGGAGGGCTGGAG AAGCCAAAGCCCACTGGTCAAGGGTCCAAAGCTGACAAGAAAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCAJCTTGACAGAGCCAGTCTCTCTGGGTTAG
558a	157 G A ---			GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGTGGAAACCGACTCCAGCCTGGAAAACTGCCCTC CCATCCCTTAGCGCCTTCTGGCCTCCGGCTGATTTCTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTTCCACACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGCTCTCCACC
187b	178 G A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCTTGGGCTGACCAATGGGTGATTACATTTAAAAACCACCAACCAACAAAAACAAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/AJAAAAATTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
187a	110 C A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCTTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAAJ/CJCAAAACAAAAACAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAACTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
1609b	146 G A ---			TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAAACAACTGCAGTCCGTTCAAGCTGTAAA AACAAGCCCAAAACCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTAAAG GATGTTCAAAGJ/AJAGGGTCCCGGCTATGTGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAA[C/T]GTGCAGTCCGTTCAACAGCTGT AAAAACAAGCCCAACCCAAAGACATCACAAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTGA AAGGATGTTTCAAAGGAGGTCCTGGCTATGTGGCACTGTAGTGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTG[T/G]ACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTCTAAGGCGAGGAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAAGGTCGTGATTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG TTTC[G/G]TGCACCTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTACATGAAAGGTCGTGATTGATTGAGCAATCTAGGGG[A/C]TATGTGACAG GGGTTTCATGCACCTGGTACAGAACACACAGGGAGTTTCACAATTTTTTTATACAAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTTCA TCATACAAGACAAAGCACAAAAGCACACCCTATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAAAATCCTAGG[T/A]AATAACTTATGTGTACTTCTTGATTTC TCATACAAGACAAAGCACAAAAGCACACCCTATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA[G/A]GACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAAATACTCTAGGAGAGCTGAAAAAAGGAAC AGATGTTAACAAAAACAAATTAAGGCTGCTGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACATAAGGGCCGTGAAAGGCATGATTGTTTGGCACACAGAGTGGATAACCA[T/A]ACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTCTGGAGAAAGTTAAAGTGTAATAATTACAAAGACTGACATGCAACTCTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAAGCGGCTGCCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCCACCATCACCGGCCCTGCCCATCATGCATCCCAATGATTACTAGCACTAGGAA GCCAACGGGAANAGGACCCCGCGCTTGT[C/T]GTGTTTAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGTGATGGGAATGAC

WI-21661	117 G C ---	---	---	GCTTAGTCTCCACCCCTTTAAATGTAAGTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAG/CJTTTAGTCACAGTCACACAAAACACTACCTTCTAAGGAAAACGTGCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25 T C ---	---	---	TCAGTTTAAACACACATTCATCAAGGA/T/CJAGATTAATTAATGTCAGGTGAGCATAAAAGGGAGATTAATAACCAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTTATTAATTTTCATGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---	---	---	TGCTTGATTAATGTGGTGTTTACATTATCCTATTTACAGATGGAAACAGAAAATACCAGCTTTTTTAAI/A/GJTAGCAATATCTATTATATAATAAATATTGAAATAACACCATAATAATATCACTAAGGAAGTAATCTAATTGTGTTGATTTTCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGIGCTCATGCAAACTCCAATCTGAAGGTGGTAGAAAACCTAGGAAGGGACAGGGATTTC
WI-22457a	112 G A ---	---	---	TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAATCACTCATTAGACAAACAGTAAACATACCTGGACACGGTTTCAGGCATGAAGGATACA/GI/CAGTTAATTAACATAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAACTCTGGGGCCAAAACCCACTGAACCTACCCAGCTGAAACACACTGAAGGATACTGGGTAAGGA
WI-21524b	97 C T ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCCTGATGACGACCTTCGCGTCATACTTATAATGGTTAATAACAGCATTCCTGTCTACCC/C/TJGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCATATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGICAGAAAGATTCTTGACITTTCTCCAAAGTTACTTCCTCCAGGGGATG
WI-21524a	35 A C ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT/A/CJCCCTGATGTACGACCTTCGCGTCATACTATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCGCATATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACITTTCTCCAAAGTTACTTCCTCCAGGGGATG
WI-22652a	32 G T ---	---	---	TTACCTTCCAAACCCAGGCCACTTTGGAGAAAGI/G/TJAGAGAATGCTATTATAATCAATAAGCCAAAGACAATAGGGACTACCTGGGTAGACCAAGATGGGCAGTCACCATACACCATCATTCCTGCCACAGAACC
WI-21703d	197 A G ---	---	---	TTTGACATGCTGCCCTCCCTACTCCGCACCTCACCTGTCTAATTTGGGACCTGAAGCTTCAGCATCCCTTCITTAGGG CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGACATAGGAGTGGTGGTGGCAGGGGCTCTGTCATCCCTTTCTCAGCACAGCACCATCTTCACCCCTCCTGGGAAAGCAGCATTTGGAGCCCTACACCACTTGTCCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGA/A/GJGTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTTGGGGGAAGAG

WI- 21703c	134 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGCTC TGCATCCCTTTCTCAGCAGCAGCACCACATCTTCAACCCTCCTGGAAAGCAGCATTTGGAGCCCTACACQ A/GJCTTGCTTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGICTGGGAAAG TGGCAGAGCAGACTAGGGCAAGGACTTAAGGAACTTGTGGGGGAAGAG
WI- 22663c	139 G A ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGTTTGCACCTGGTGCACTTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTGAATGTGGGT
WI- 22663b	55 C T ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCACTGGCAGGTGAGCCGGCTCGCTAATCTTAA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGTTTGCACCTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTGAATGTGGGT
WI- 22663a	38 C T ---	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCACTGGCTGAGCCGGCTCGCTAATCTTAA TTCCAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGTTTGCACCTGGTGCACTTAC AGCGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTGAATGTGGGT
WI-22668	99 A G ---	---	TCTTTATCCTGCTGCCTGAGTATCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATT CCAACCTAACAAATAGTTTCTGTAATATTA/GJTCTAGTCCATTTAGATTGTGTAATGATCTAA ATGNGTAAACCATTTAATACAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACTTTTATT
WI- 22631a	52 T C ---	---	AAGATATAGTGCAGGACAAGATTGGTCAAGAAATCCTGGCTCAGTCTGAT/CJAGCACCATTTT CAAGTTTAGGCAAGGTATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACC TATGTACCATCATAGGGTACTTGGACAATCAACTGAAATTTTT
WI-20258	157 G T ---	---	AATCCACATTTACGGAGGGGGAACAGCCTGCCATGTCTGCCAGGCTCACAGCAGCGCGGCTAC TCTGCTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCGTAAGGCATGACAACG GGAGCCCGCGGGGTGTTTCA/G/JCGCGTTGACGAGGTGCTGGCTGGCAGCGGCGCTCTACAGA AGGAGGGAGCGCAATTCACAGCCTCTTGACGTAGTTCCGGGGAAGTACC
WI-22714	212 C A ---	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTTACATTTGTAGAGAAAATCTAGGGTCT ACTAAATAATCTAGTACTGTTTCCACTCTCCTGTAACCTGACAGGAGTGTGTGGGAAACGAAAGT CTGAAAGGATTCAAGGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/C/ATGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI- 22734a	44 G A ---	---	TGGGGCTACTTTAGATGGGATGGCTCAGGGTCTGGGAAGCCCTG/JATCTTAGAAGACATTACCCA AATGATGAGAGGCGAGCCAGTCGTCGAAGCCATAGTTTGGATGGGAGACTTTCCGGCAGAGGAAAT AGCAAGTGCAAAGGCCCTGAGGGAGAAATGAACTTGGGCTTGCTCTACAGGGTGAAGGGCGCGGT NTGGCTGAGGTTTAGTGGATG

WI-22724	117 A G ---	---	TGATATGATGCTGAGATTTGCTTCCAAATATGCCATAGGAAGGGAAGAGTGTATTAGAGATATAGGA CAAATCAAGATTGTCAAAATGTATAGTAACTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAATT
WI-22750	48 G A ---	---	TGTAACCTGTGTTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCAATCTGACTGTGCT
WI-22775a	60 A G ---	---	TGCTGTTTCTTTAGTTCATGACGTTTATCACAATGTGCTACTGTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAATCCCTAAGGGCAGCAATAATTTCTGTCTTTGAATCCTTCATTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACAGGTATGTAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---	---	CTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAGTCCCTGAGGGAG CCTAGTCCCTCCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	TCCTCGTGTCTTGAGCCCTCATCCCCACCCCTCCAAGCCCTCATGCCACACACACCGTGTCCACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCAATCCAAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGGAGTGGAGATGGCAGAGATGGGGTGGAGCCAGTGGCTGTGGGTC CT[G/A]TTGGCGTGGTATGTGGGGGCCAATCCTGAGGCCAGAGGTTCA
WI-21031	31 C T ---	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCATTTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATACTGCAGGAACACTCAGTCTCTTCAGCAGCCCGAGAAACACACACA
WI-21314	122 A T ---	---	CCATATCCAGTCTCTTTGAAGCTTTCTATTGACITTTAGGGTTCAGTTATTATATCCTTTTACTACTAT GACTTTCAITTTGATTTTTTATTTGTTCTCTCCATTTCTGTCAAACCTTTTC[A/T]TTTGTATTATAA ACTGTTTTCTAACTTCACTTAATCTCTAICTGIAITTNCTGTAGTCCCTGAACCTCTTTTAGAGG AGCGAGCATCAGAATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCCGAGAGCTTCT GATTCAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCTTAAGTGTGCAG ATGCTGCTTGTCCCGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21186	95 G A ---	---	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAAAATCAATAACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGTCTCAA AGTATGGCTTCAGACAAGCCCATTTGCATCACCTAGGGGAATTGCTAAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT
WI-21187a	94 A G ---	---	

WI-21190	39 T C ---	---	---	TTTTCCCATACCAATGCACCTGTTTGTATAACTATT/CJGTGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTAATTATAACAAATAATTATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTAGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTAATAAAAGCTT AACACA
WI-19937d	186 G A ---	---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGIGTTCCTCAGCAAGTC/GJA/TCCAAACCTTC CAAAAGAAAGCAGTCATTGAAAATGCTGACTTATGCAATTGCCTCAGGAAGAA
WI-19937c	185 C T ---	---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGIGTTCCTCAGCAAGTC/GJA/TCCAAACCTTC CAAAAGAAAGCAGTCATTGAAAATGCTGACTTATGCAATTGCCTCAGGAAGAA
WI-21117b	227 C T ---	---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCAGTAAATCTGTTGAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAATACATTTCTGGGG TCCAATCACATACCTCAGGTTTCAGACTCCTAGTCCCAATATCTCAGTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTC/TJTTCTACTGAATCTTGGTGGGAG
WI-21122a	42 C T ---	---	---	TCACTTTGTATCATAATCCCCTGTAAAGCTAAAGTTATTCAC/JTTTAAACAGGAACTCTGTTTTC TTATTCAAATGTCACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACCTGGAATACT AAACAAATCTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTTCACAGAGAGCCTATTGTGGGTTGCT
WI-21254	53 A G ---	---	---	CAGTTTGTGTACAGGAAGGGCCCATGAATGTTGGCGGAACTATCCACAGGAG/JGJCAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	---	AAGGAAACTGCATGGGTACAAAT/G/JTCCAATTACATTAACAAGGTGGGAAACGGGTCAATTCT TGGCCTGCTCCAGAACAGGGCGGAGTCTATGCACTCTG
WI-21059b	181 T C ---	---	---	GGGACCAGGGTAACACCATTAAGCAATATCCGTTATCAGCCTTATCTTCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTCCTGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTC/JATTTAGCCAGGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63 C T ---	---	---	GGGACCAGGGTAACACCATTAAGCAATATCCGTTATCAGCCTTATCTTCCACTGAGCCTGG/JTJ GAACTACAGCTGCCAGCATTCCTGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT

WI-20442	37	T C ---	---	TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTTAAACAAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43	T C ---	---	GTGACAAGAGGTGAAGCAAGGGACAAGGGGCAGCAGGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57	T C ---	---	ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGGAATGCCTACATCTGGAATTT/CJATTAC ATCAACGTTAAATTTGTCGACCAGTCTTCATTGCTGATCACATTTTGATAATGACAGATCCAACAT GAACTCCTGAAGCAAATGAATATTTACCTTGCTTTCATGCAAAATTTAGGGACCAAACTCAAAAGG TTTCATCCATGCTGGACACCAGATCTAAGGAATTTGTACAGGGATCTCT
WI-21149a	167	G A ---	---	AGGACCTGCTCTCACACGTTCCCTCACCCCCACCAGCTTTTGGCAAAGATAGTTGACTAAATACCACCT AAATAGTGGCTTTTTTTTTTAAACAATGACCTTATTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCAACTGAAAGCTTTTACAC[G/A]TGCTTCAGAATCGGCAGTATTGCACAAATGGTT TGGGCAGGTTCTGTGGTTAAACATGGGATGGAAACCCAGGCTCTACCTG
WI-21376b	188	A G ---	---	GGTGCAACTTGGAAATAATGGTTTAAACACAGGATAAGCATTAAAGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGTCCTCGTGAAACCA GACAGTGAATCTGTTCCAGCCCAAATCTGCAGCATTAGGGATGAGTTCTC[G/G]GAAGTGATTCT GAACTGAGCACGCACTCATGCTGCATGGGAACTCTGGGAGAAGAGCCT
WI-21382d	125	C G ---	---	CCATTGCAGTCCAGAGATGAGAAACTGGACCAGAGGCAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTTCTAAGATGGAGAAGTGGGGGGGTTGGATCCAGTGGGATNGGTCCTCC[G/G]AGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCAGTCTGATGGGGAGCAGAAGAGTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGAC
WI-21437a	201	G A ---	---	TCCCTGAGGTTGGAGTCTAGCATAGTCCCTCCCTCAAGAGGGGACAAGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCTTTGGGATGGAAGTTTCTGGAGTCCCTCCATT CTATTCTGTGGGCAGGAACATGCCAGGGCTGCTGGTAAATGGCAGGGTGCACTTTACCAGGG[G/G] A/CAGGCATAGTGTGGCCCTGNCTGCCCTGGGGGCCACCTGGGAACAGT
WI-21202b	156	A C ---	---	CAAAATAGAAATTCCTTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAAAATGGTCACAATATATTTTTTAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCAA[G/C]GTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A
WI-21202a	61	T C ---	---	CAAAATAGAAATTCCTTTGTGAGTGGATTGACTTAATTTATTTCTGTATAAGCTAAATATGTTGATGA TCTGTTTTATGAACATGATTTTATAAAAAATGGTCACAATATATTTTTTAAGTTAACTGATTTATTGA GGGAGGAGGAGAGATTGACCAAAGTCTACATGCATAGACAGTCTTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCACTTGAGTACCTCATTATGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA[A/G]TCCAAAGTCATCTAATAATTAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCACTTGAGTACCTC[A/G]TATGGATAATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATAATTAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTTGCTTA
WI-21399a	75 C T ---	---	GGATTGAGTCCCAACTTGATCTCAAAATTCACCTTTCATGTAAACAAGCTCATTCCTCTAAAGTT TCAGTTT[C/T]TCACCAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGIGTCCCTAGGACTAGGTAGGATCTCTCTTGGCTTTCTGCC TTACCTAGGCATAGTGCCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI-20329a	68 G A ---	---	CGATGTCTGCTAAGATAGGAGGTTAATCTTTACATGGTGAGTGGTCACAGAGACAAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAACAGTAAACCAATCAAAAAGAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATTCAAATGTACATGTAAATCCAATTTAACAGATCAAAATGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTCACTTTAAAGAACATTATAAAGGTAATT AAACTCTAGGTGTACTTAT[C]ATGGAACTAGTTTATTTCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAAACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGCGCGGCTCCAGCTGGGTTTCCC AGATGCAACAAT[C/T]GGCGTTCTGGCTTCTCCACTGTGGGGATGGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACAGGGAGGACAGCTGCTGGCAGGACTAATAAACCTTCCACCTGGCCATGGTGGTGTT CTCTATGGACCGAGGCCCTGAACGCGGCGCAGGGAGGGGAGAGAAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTCTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGCAGTGGCTCTTTGGAGAAGGCA[G/A]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTCTCCACCCCTATTTCCCTCCCTGAAG

VI- 21475b	117 A T ---	---	TAGCCCTCTGCCAATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTC/A/TJCTTGCTTACTAAGCA CAGAGTCTGAAGCTTGGACCTGGCAGTGCGTCTTTGGAGAAGGCCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCCTATTTCTCTCCCTGAAG
NI- 20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAAGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTCACGTAAAGTTATCACCAGCACTCC AGCGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC/A/G/ACATAACATTGGTAGAGTAACAACAACCAACCAAGCCTAAATG
NI- 20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAAGG CTGTCTTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGTCACGTAAAGTTATCACCAGCACTCC AGCGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAACAACAACCAACCAAGCCTAAATG
NI- 19941c	71 C G ---	---	GAGCTCAAGGGAAGACCCCTTACCAGATAGGGAACCTAAGGAGGCTGGAAGGAAACAAGGTGAAA GGTATC/G/GGTCTGGTGAGACAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGCAGGCTGAGGAAGGAGATGGGGACATTTCCCTATCCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATNTGGAAAGGAGAACCAAGGACAGAGACAAAGCG
WI- 21552b	166 C A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATCGCATCTCTTCACCTCAAGCATTTATCCATAGTTTACAAAGAA TCCAAGTACTCTTGATTATTTAAATGTG/C/A/AAATTAATTTATTTGAATTTAGTTACCCC ATTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTTGTA
WI- 21552a	66 G A ---	---	TGGGTACATGGACAGATGTATATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATCGCATCTCTTCACCTCAAGCATTTATCCATAGTTTACAAAG AATCCAAGTACTCTTGATTATTTAAATGTACAAATTAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGT/C/G/JAGAGAGGGA AAGAGCTGGTGCTGCTCTGGAGGCAACGTCCAGTCCGGGAAAGCCACTCGTGGTCTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTCGCCCAACAGGCGAGCCTCGGGGCCAGAGATGAGATATGCTGTAA TCCAGTACAGGGGCTGCGTGGGTGCCCCAACAGCTCTCTTTGGGGG
WI- 21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACCTGAAAACCTCTTAAAGGCAAGGACAAAGCAACTTCCATT ATTCTTAGTTTAGACCAGAACTTTAATTTTATTTATTTCTCTTTAATAAAGTGTCAAAAATACACCAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCGAGTGTA[G/A]AGTAG TATTCCTACATACCACAGTATACAATGATGCCTTCTGCGAGGTTTAGGAAC

WI- 21514b	133 C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGACAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTGTGCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCA[A/G]TCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCTTATGACAGGAAATAAATGAGG ANTTTAAGGCTCAGATGGGGTTAAGGGTGATTGTGCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	ATGAACACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGATCATCTACCTGATGAGGGTACTT
WI- 19576a	113 A G ---	---	TTTCATCGGTTCTTAATACAGTACAATCCCTTTTGTGTAACAAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C/A/G]TCTAGTTCAGTGATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAGGAGTGGGCACCTTGGAAAGTGACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACCAGAAAGTTCTTGGGCATGTGATGGTAGGCCAGACCCCTTTCCAA GGGAAT[A/C]TACTACACTAAGCCTACACTGTACTGTGAGAGTCTGTTGGTGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTCCAGANTTCTAAGGCCAGCAT
WI- 21574a	235 C T ---	---	AAACCCAGAATTTAGGTACTTTTGTATTATGAGGAACTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTAATGTCCTCAGAGTCACTAGGGAGCCATT GGCAGGCCAGGGAATTAAGTGCCTACTTCTCTTCTGTCTGTCAGGTGGGA
WI- 21644c	151 T A ---	---	TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGGTCACCTTAACCTTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCACCATANTATTTAACAGACTCAAAGTGATACATAAAGCTTG TTTCATAAATAAGGGA[T/A]TTCAATCAAGATCCATGGAATGATGCAGTTTAACATGTGTCTCAGC TTGCCTACTGACCACCTTTCCTTTCTTAAATATGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---	---	TGTCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTAT[C/G/A]TTTTAACA AACCTCATTATGATCACTGTGCAATTTTCAGTCACCTAAAAATACGGAACCATGACTATTAAATAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAAGCTTATAGA GAACTTGCAAAAAAGTACAAGATGGCTATTTTAAATTTACATACATATTAAGATAAGGATGGACT CTTTCACTGAGTATTAT[C/T]AGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATATTGGCCAAAGGGAAGGTAAGGATGGTACTGTGTGGAACCGGA

WI-21981	61 T A ---			TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCCTTGAAGAAAAAAATTAJGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---			TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGGTGAACACGCCCTCTCCACTGCT TACTGTGTGTACCAAGAAAGGCAGAAAGCAGCTCACCCAGCCTAACCTGGCC[C/T]TGTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACCTGCGGAACCTGGGATGCAGGGAGAAAGCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---			TGGAAGTAGCCCTTCTGGACAGAAAGAATAATTTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGTAGTTTCCAGGGCTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGGATCTCCCC ACAACTTC[C/T]TCCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33 T C ---			TGGAAGTAGCCCTTCTGGACAGAAAGAATAATTT[C/G]TGGTCCATGTGGTTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTGTCTGTAGTTTCCAGGGCTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGGATCTC CCCACAATCTCTCCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81 C A ---			CAAACCTAGTCACTCTACTGATGCAAAATGATTGGAGGTGCTTCTCCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[C/A]CCTCTGCTCAGTTTCAGGGCA
WI-21760a	35 A G ---			CAAACCTAGTCACTCTACTGATGCAAAATGATTGGAGGTGCTTCTCCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCAACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---			TCTGCCATATTGTTCCAGCACCACCTATTACTGTTATTATTTCTCTTTGAGGAAAAACCCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCCTAACTCTATGGTTAAAAATCCTTTTCTTACCAAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGAGGGAAGACTGAGATATGTTTGCAGAAATTTATCTCTAC[T/C] AGAGACAATTCATAGTTTATAATCTTTTTCAGGGTTGTGCTTTACTTGGGGGC
WI-20934a	72 T G ---			CCACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGGTCAAAATATTCAAAATGGCCTGGCAGTGTAGTAAATTCAGCAGAC AAACAGCATGAGAAAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCTNTTCCCCAGGAGA
WI-21561	55 T G ---			TTTCCATTTTATTCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCTT/GJCCTCTTAAC CTCCTCCAGGCAAGAAAGGAAAAAGTGATCATATTTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAATATATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTATCTGTTTAAAAAGATTTTGGATGATGTGTCCTCCCA

WI-21961c	200 T G ---	---	AGCTTGGCTTGAAATTTGGTACTTACTACCTTGAATCTCTTTATTATTATTACTTTATTTTCCGTAAATTTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGCATTTGTGTGATTTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACCGGTCTTTATCCCTCGCCCTT/GC/TCCACTTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGC
WI-21961b	73 G A ---	---	AGCTTGGCTTGAAATTTGGTACTTACTACCTTGAATCTCTTTATTATTATTACTTTATTTTCC[G/A]TAAATTTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGCATTTGTGTGATTTGGTGACCCATTACCCAAAGGAGTATACACTGCACCATACCGGTCTTTATCCCTCGCCCTCTCCACTTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGC
WI-21956	26 T G ---	---	CCCACTTGGGTCTCTTCAAGTGAAT/GTTCCTTTTCGTTCTTAAAGCCTTTTAAATGAACCTTCCATTCCTGTTCTGAACTTGCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATCTTTCTTCTGAGCGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTCGACGCGGTAACTCAGGGTAACTCCTATCTTCCACCGGTAAACAGGGGTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	CAACATACATTATGGCTGCCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACATATTTTTGTAGAAGCATGAGTGAGAGTGTGTGTGTGCGCGCGCGGACGGCATGGCACTGAGGGGATTGCAATGGG[G/A]AACAGGATAAAAAGGTATAAAAACTTGGTCCGAAATCTTTGCTTATTAAACCTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	TATACTGGTTTTGGTTACATGGATGAATGTCTAATGGTGAAGTCTGAGATTTTAGTGTAACCATCACTGAGTAGTGATGATGACCAACTGTAGGCTTTTATCCCTTACCCTACCTCCACCCTCCCCATTTTGAGTCT/GC/CATAGTCCATTATATCACTCTGTATGCCCTTTGCATACCCATAGCTTAACTCCCG
WI-21139a	165 T C ---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTTCAAGTCCCTGTTCTGCCA CTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTGTGAAATGGGTACAA TGTGGTCAAGCAGTAAAGGAACTAATACAT/GC/GTACAGCACTTCAGCACAAAGCCTGGGCACACAG
WI-20317b	217 G T ---	---	CACTGCATGGAAATACACAGGTAAACATTTTAAACAGTGGGACAAAAATTTTAAGTACGTGGCCAGC TGTGGTGTCTTGTGGTCATTAAAGACAAATGTTAAGANTCAGGAGTACTTAAAGTCTAGTGGTTACA AATTTGTCTCTTCAGTTTTTCATTAAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAAA[G/T]TATTAAATTAATGCATATTTTGAAGGCTACTCT
WI-22082e	179 G A ---	---	CAGGACTTGGTTTGTGTCCTCCCACTGCACATAAATGTCCCTTTTGTGAGTATTGGTTGTGGCG TTTTCCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTGCTTTATCCGGATGACGGAGG GTACACGGGGGCTCGCTCAGTCCCGCGAAGGACGTATTC[G/A]CTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGGCCACGATTTCAAAATCCTCTTTGCTGCAACCTCT

NI-2082b	67	CT ---			CAGGACTTGGTTTGCTGCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATTGGTTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCGCTCAGTCCCGCGAAGGACGTATTCGCTGAACTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAATCCTCTTTGCTGCAACCTCT
NI-20993	139	AG ---			AACACAACTCCATGCTTTCAAGATCCCACACCCAGATACTAAGACATATTAAAATTTACAGCAAT TAAACAGTGAGTTTGGTACAATAACACATATAGCAATGATACAAATTAGGGGAAAAAACCCCTGG GCTTCT/A/GJTAACAAGTGAGTATACATTAAAGACAGATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGGCCATTTCAGGCTTCCTAGCTCATCCACACATCACC
NI-21723b	125	AG ---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCA/A/GJCAACA GCATGATAAAATAATTCAAATATGTAGAAATATAGAACTCTAGGACTAGCTGGGAACTCGGAAATC ATT
NI-21723a	82	GA ---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/GJACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAAATATGTAGAAATATAGAACTCTAGGACTAGCTGGGAACTCGGAAATC ATT
WI-22132	99	TG ---			CAACAGATGCTTGAGCCAAAAAGCAACATAGGCGAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTT/GJCCCCATTTCTCTAATCTCTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCTATAGGAATGCCTCTAGTTTAAATGCTGCCCCAAACA ATACTAACCCATTGAAGGATACTATGGAACCTTTAAATGGGACAGTGGG
WI-21006a	106	AG ---			TGACAGATCACACCACATTTTGTGTAACCTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCCTTAAGAACACATACACACATGTGCACACAC/A/GJAGAGGCAAGTACAAAAATGTAACC CCACCAAGTGATGTGAATGAAAGTGCAAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAATAAACAGAAAGTGCTAACTGCCCTAGGCCT
WI-21761b	138	CG ---			CTGAGGCCTGCTTAACCTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAGATTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTTACATCTTCTTCTGCCAGTTAAACGTCGCCGTGG CTC/GJCAATACACACCACCAAGCCAAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	GA ---			AATGAAAATGCCACCCAGAGGTTAAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATCTCCATGAATTAAGCTGTGTGCTCAGCTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG/GJAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT

WI- 21079a	50	G A ---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG[A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACA TAACCTAGGCCACCCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACATCTGCCAGGGTAATAGGCATGGGCAAT
WI- 22129a	45	T G ---	---	TCTGTAGATTTTAGCCATGCCATATATTTAACTTTAAGGAAAAG[T/G]TTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGCAATAAGTTAGCTCTAACAGTTAACATTGAAGCTTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTTGCAAAATCCAGNAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79	A G ---	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCCAAGAAGGACTCGGAAGATGTTGATCCAGGGCAGAGT GAGGGCAGAC[A/G]GGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCACACCCACCACTCACC CAGCACACAGGCACACGCGCAGGGCACACGACACACGNTGCACTCAACACGC
WI- 18916b	42	C T ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI- 18916a	35	G C ---	---	AATGGCATCCCTGTGATACCAAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI- 19828c	200	A G ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAACAA GATCAGAGGTGCTAAGTGCTGTAGCCTAGTGCCAGGNCCTTCTGGCCCCAATTTCTGGTTCTCCCCAAG CCCATGCTTCTTCCACTTCTCACAATCTTTACTTCTCTCTGACCCTCACCACCCAAAATTA/G JCTTTTAATCTGGAAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI- 21863b	47	C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCCT[C/T]AGCTGCATGCCACCCCTC ATATCCACCCCATCCCAAGCCTCCTGCCCCGACACCCCAAGGCTCCCTGCTGTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACACAGCATCT
WI-19860	51	C G ---	---	TTGACCTAAAGCCTAGCATAAATAGCTAAGTAGAATGTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTGCCATTACCCATAAAATGGTGGGATCTACCTCCCT CCTTGCAATTTGAGCTGNNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI- 19889b	80	C T ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACTGCAGGGCAAG AGGAGTGAGGGG[C/T]ACAGCATTTATTTCCCTCTTTCACTCCCTGTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTCTTGGCCACAGTCGTAACATTCG

VI-9891c	172 C G ---			TGTTGGTCTGAGAATTCACAGCTTACTACAAGGAAGCTGAGAATTGCTTGGTGGCCCCCTCCCCCCCGG ACTCCTCTGTCTCTGGGAAACGTGGCTTTGNCTCCAGACACAGTGTGATGCCAGCTCTCCTCAGCGG AGTCCCGATCCCTCAATTGGCCATCTGTCTGACTC/G/GJGCTCTCCGGGGCGTGGGGCGTGTGTGT CAGCAGCGGGCGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
VI-0155a	81 C T ---			GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCACGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGG[C/T]GCAAACTGCTTTGAGGAAATNTCCCGAGGAGGAATAAACTAGAGACGC ACCTGCTATTTACCATATCTATGGAGAATACAGCTAATGAAGTGTGGCAGAGCTTGGCCGTGTGA GTGCCCGAGGGTAAAGTCTCTCTCTGTCAGTCCAGAGCAGAGACTTCTC
II-0270b	91 T G ---			AGCCATACAAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAAGGATTTATACCGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTGTGTTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
VI-0270a	53 G A ---			AGCCATACAAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG[G/A]TCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACCAAGATTTATACCGGTGGCAGCGGTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAGGATGCT GGGTGATCTGTGTTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
VI-20622	130 T C ---			CCACTTTCAATATTTTACAAATGCTCACGCGAGCAAAATATGAAAGCTTCAACACTTTCCCTTTGTA ACTTGTCTGCAATAAATGCAACTTTTAAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTACTCATATTTTATCATATAGCTTTTATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCAAACATCTGTCATGCAG
II-0768b	190 C T ---			TCCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCAGGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACTTA CAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATCTGCTGGGA[C/T]CAGGGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
VI-0768a	71 C T ---			TCCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGGCTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGGCACCCAGAGNTCAGCACACATCTGCTGGGACCCAGGGACTC GTAATTCGCTTGGTCCAACTCCTTCTATGGGGTTAGCTGCCCTCATTC
VI-21909	153 A T ---			TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAAATTTATCTCATTTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTTGTTGGTCATCTTTAAAGAAA TGTCCTTAACATACCAAAG[A/T]AGTGGGAATCAATAGAATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACTAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---	TGTTGCTTTGGTTGTTTCTGGAAACATATTGGAACACTTGTTTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCTTTTAATAAGGTCATTATGAAATCTGAATTTCTA/GJTTAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCCTTGCCGGTGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	CCAAGGATGAAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTATG AA/C/TJGAGGCGAGGAATGGGCATGGCGCTGCGGTACCAAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	GGGAGGCATCATAGAAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACATAGGCCTCTGCAGGCTCTGGTTG/T/CJTTCATTTGCAAAATAAAACCCA GACCGGGTCATCTTTCAGTCCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	GACGTCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGCCCTCTAAGCACCCG GCCAGTAGTGGGAATGCCACATGCAATGGTGAGTGGGATCTGGGGGGGTGAGGACCTTGCTTTT /C/TJTTCCAAATCTCTCTTAGCCAGAACTTTGCGAGAGCCCTTNNATTTCTCTCCCTCTATTCC CCTCCTTTCCCAATGTGTAAGTCCCAATCCAGACCCCTCCAG
WI-22292	53 A G ---	---	CCAGTGAAGGGTTTACAGCCATAGTGAGGTTCCCCATTGCTCAGTACCAGA/A/GJTTTGAGTAC GGTCGTTTAAAAAATACCTATCTGACCACAGTGGA
WI-22387	186 C T ---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACAATCTATACCCACTCTGGCTCTGAAAG GCTTGCAACCAAAATGGGCAGCTGGGGCTAAGGCATATTTAAACAAAGGCTCCAAGGACCCCTT TCACCTGGGTCTAGCATCCAGCCTCTCTCAGCAAGGCAGGATTGTGGT/C/TJCTTGTGTCTTCTG AACAGGGCCAGGGCAGCCAGGCATGCCATCACTGCAGCACTCAACCT
WI-22395b	127 A G ---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTCTTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAAGGGGGCAACTCTTTAAT/A/GJAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	TTTATGGCTCCTGAGTCCCTTACCAGCTACACTTTACCTTTGTATCTATAAAAGTGAATTTAGAGT AAATACATTGGCTGAAGTCG/A/CJGATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGGCAAGGTTCTCAGTG
WI-22419b	67 T C ---	---	CCCTTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGNCTGCCCTTCCAGGCACAGCCAGTGCT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	ATTTTCCCTTCTGTGTTTCGTAATTTCCCTTTTGTGCTAGTAAATNAGCAATACACTGA/T/CJTGGA ATCTGCATGATTAATAACATTAAACAAGTTCATAAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCCAATTAGGTATCCCTCAAAATTCACATTTCTCCTCTAGTT T

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WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACACAGCTGATT[G]CAGACATTGCCTGTGCTTCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGAGTTCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T[C]GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTAGTCCCCAGTCGAGGGTGCACTTCTTCTTATCTTGCTTAAGCCACTTGGGT[A/C] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAACTCCCTGGAGGGAGGCTTCTG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAAATACAGTAC TTCTTTT[C]GAAAAAATACACAATGGGAACCTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCTGGCTTTCTGCTCCAGGCACTGAACA CAGTCAGGCTCTCTAAACACTGGCAGGGACCTCCCCACAGCC[A/G]CCCCACAGGGTCTCTGTT TCCCAAGTCTGATGGATTGAGCAAGACCTTCACACATTACCCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTGGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTAGTCAGAAAGTCTCATGGACTTTCTTCCTAAG[C/G]TGTCTATGATCAGAC CACTCTCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAATTTTCACTATTGACTATACAGAG TCTTCAATTCCTCAAAACAGTTAATAGTAACTTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT[C]AGGNTCCTGCATCATCTCTTCAACA
WI-22250b	132 C T ---	---	ACTTGCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTATTATGGGCTCTGCTCCTCTGCTGTGTTATG[C/T] GGANCCAGGAGTGAGGAGAGCCGTGGAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTCAGGCAGGCACTTCTGGGATCTAAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTATTATGGGCTCTGCTCCTCTGCTGTGTTATG GGANCCAGGAGTGAGGAGAGCCGTGGAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCATCTCTCTCCACACCTCCAGGCCACCTGGGGCCAGAGCACCTCATGCCCCAGCAGCAC CTACGTGGCCGAGTACGGACCCGCTGGCCCCAGGTTCTCGGCTCTCAGGACGTCCTCCAGCAAGTGA GCCACAGAGGTTTGTCTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTG[C/G]AGTGTCTC TTTGACGGGGCCGCCGTGCTCAGCTGCTCTCTCTGAGGAGGTGAGGAAGGAGGT

UTR-						GCAGCATCCTCTCTCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCGCCAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGA GCCAGAGGTTTG[C]/TJGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGCTTC TTTGACGGGCGCGGTGCTCAGCTGCTCTGGAGGTGAGGAAGGAGGT
stFIBBb	412 GC	---				GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCCCACGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCAAGTT
stFIBBa	341 TC	---				GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCCCACGGCCCTTGCCACTGTCTCTGGCCCTCTCTCTGATCATGCCAGG TTTGACCCAGCCTCGAGTCTCCCATGTTGTAGTACATTTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCAAGTT
stGLV2	61 TC	---				GTCACAAGAGGCGAGCGCTCTCGGGACGTCTCCACCATGGCCTGGGCTCTGCTGCTCCTCAGT/CJCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGGTCTTGGGACCTCTGGGCTGATCCTTGGTC TCTGCTCCTCAGGCTCACCGGGGCGACACTGACTGACTGGCATGT
stSG1001 7c	70 TC	---				GTTACGGCTCATCTTGAACCTCCTGGTCAAGCGATCTCCACCTCCAGGCTGCCAGGGTGTGGGAT TA/TJAGGCATGAGCCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33 GA	---				GTTACGGCTCATCTTGAACCTCCTGGTCAAGC[G]/AJATCCTCCACCTCCAGCTCCAGGGTGTGGG GATTATAGGCATGAGCCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63 AT	---				TAATGATAATTAGGGCATCTTCCACACGAAGATGACACAATTGACCCAATATCATTGAGGC[A/T] AACAGTTTGGGCTGTTTTCAGTAGTATGACAGTGA
stSG1009 6	36 GC	---				GTGGAGAAAGATCGTCTTCTCCTCCCTCCCATGACC[G/C]/GGCTTCCCGGGCACCTGTGGTTTTCC ACCCGAGACGGCCTTTGTAGGACCCACTGCCCACTCCGCTGCTGTGGCTGGTTCGGCTCCTCTAG GGCTCGAGTGTTAAG
stSG1011 8	107 CA	---				TAGGCTTAAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGCTGAGGGGAGTACCCCTCCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATTTCTTGGG[C/A]/CTCAGCCCTCAGTTCCTTCATTCC ACCAGGCCGTGCTTGTGATTTTCTCCCTCCAGTGAG
stSG1012 0	89 TC	---				TAGTAGGTAAGAAAGCAAGGAGGATTGCTTATCGGATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTCACGAACACTTAATA/T[C]/GTTGTGTATCTGATTTTATCCTCGTCTACAAATG
stSG1017 8	42 CT	---				TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAAGTCCG[C]/TJGGGAGGAGAAAGTGAACAGGAA TCGATCTTTGCTTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTGGC

stSG1019 3	136 G A ---	---	GGAACAATACTACCTAAGGACAAAATACTATTATAAAAAAAGTCTTCTAGTGATATATTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAACTTTTAC TIG/AJTITGAAAACAGAGATTTAAGTTGCAAACT
stSG1020 2c	143 G T ---	---	AAGCTAACTTAGGTGAATGGTGCCACTCAAAGGCTTTCCGAGGGAAGCTCAGTCTGGCTTGGGAGAGTCAGCCTTGGTCACCTCATACGGGGCTCCAGCTAAGCGTCAAGGAGCAGTCCCACTGCTTCTCGCTGTCA[GT]CAAGACCACAAAGGCAGATGCCCACTGCTGCCCTTTCCCTTGTCTACTTTCT
stSG1020 9b	75 A G ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAAATAAACTAATCTCTTAAGATCCCACCTTATTTTTA[AG]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 C T ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC[GT]AAATAAACTAATCTCTTAAGATCCCACCTTTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 T C ---	---	TACTAGACATGCAAAATGAGAAGATTACA[GT]GTGAATATTTAAAGAAGTTATATTTGTTTGACATATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 A C ---	---	ATAGGTTTCAGGAACAAAATCATTAAATGGAAAAATGAGAAGAAATCTTTATTTTGGACCAATTTTAGGCACTTAAGAGTTTCTTTCTCTCCCTTTCCCTTTGATCA[AV]CJAGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTTG
EST10915 0	123 A C ---	---	CTGTATTAATTAAGAAGGCACCTATTAAATGAGGGACGGAAAAATCTACCTGTACACAAAAATTCGTACTTAACAGCATCTTCAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG[A/C]ATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166 T A ---	---	TTTTTTGTTAAACCAACCCCTGAAAGTTTCCACATGTGAATATAGATACAACACAGTGAACAAAAATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCCTATACACCAGTAAACACAGCAGGGCAATTAGTCAATTAATAAAAAATAGTACATGTTA[GT]GTAAATAAAATTTAAATTTACAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGGAGGAGTAATCCTGG
EST14096 8	71 G C ---	---	GGGATGTATATTACAGATAACACAACCTACAATAATACCATCAGACATTGAAAACTAAGGCCATTCTGTGA[GT]TATTTTAAAACTTGGTGTTTTGCACATAATGATCTTAAAAAATAATGAATTAACCAAAACCAAGATTCTCTTCAAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 C A ---	---	TGCAAAATGTGAGAAGGCAGCAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTGCGCAGGGATGCTTAAGTCTTCTCTCTGGCAGAGACCCGAGGTGCAGAGATGATCTTCTCA[CA]CCTTCCTCAGGGTCTGGAG
EST22555 7	60 G A ---	---	TCAAGCATGTGTAAGGCACCTGCCCCGCCAGACCCCTTCTAATCTTGCACACTGGAAGGT[GT]AAAACTGGGAGAGAGAAGACACTCCCTCCCTAGCTTCTACCTGGGACCCCTCCAAAGATGAGCATTCATCCTTGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---			GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTTGGGCTCTCAATGCA ATAGAAA[C]/TTGACATGGGGCCAAAAGACTTCCAGACAAAAGCAGCGGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---			CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCCCTCAGGCTGTCTACTCA[A] GTTGGTTTCTAGCCTCACTCGCACACAGGAAGCTTGGAAITTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56 A G ---			GAGGGGAACCTTCAAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGGCAAAAGTCA[G]CTATGG GGCCAGACTGAGGTTGGAACACACAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGGAGTAGCCAT
STS- R37410c	201 A T ---			TGTGACCATACCAAAACCTATGCAATAAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGTATG T[A]/TTATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---			TGTGACCATACCAAAACCTATGCAATAAAAGAAAAAATCCTCAGTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGGA ATTTATG/TJGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410a	48 C T ---			TGTGACCATACCAAAACCTATGCAATAAAAGAAAAAATCCTCAGT[C]/JTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTTTTTGAAGTGTGAATAAAAGTTCATAGCATTTT GGAATTTATGGTTTGAATAAATACAAAATGTGTGATCTCCTGAGACACATTTATAACATTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R42778	74 C T ---			TATCGTGGGAAGTCCAAACCTCATACTTATGCTGCTTTTCTACTTGTCTAATATTGGATGCTTCTTGCCA GGCTC[C]/JTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA
UTR- 04350	125 C G ---			CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCCCTCCGGGATGGTGAAAATGTTCCGGACCTAGATA[C]/GTTGACGA AGGTAGCAGCACACTGTGAGTGCACATAA
stSG1026 6	55 T C ---			GAAATAAACTAAAC TGCAAGCAAAATCAGTGTAAATAAGAAATTGTTCTTCTGTTT/CJGACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1028 2	70 T G ---			GTATAATTCAGCATAAGCCAAAGCCTTTTAAAATAACCAATACTATCATTTTATGAAATCTTTACA AGA[T]/GJAAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C/A ---			CACTTTAGATATGAGGAAAATGGTTTAAATGGACACAAAAGGAGTCAGCCACGTTGGAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGTATATGCAATAACAGCAAAATAATTTTTCAC[T]C/A/JTG TCAATGCCAATGCATTGAAAGGCCCAAGAAATGAGAAAAGGATAACAAACTTTTGTATAAAAAGGTA AGAAATTTCTGTGTG

stSG1033 1b	116 T C ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAAACCTGTCTAGGAAGCCTAGACCTCAACACCAACCTCCA[T/C]GCATTTCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTCGG GCTCCAAACCTGTCTAGGAAGCCTAGACCTCAACACCAACCA[T/C]CACCTCCATGCATTTCCTCTTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---			ATTGGCAAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAAATCCTCCTCTTG AAATTATGTTAGGCCAGCATGGTAGCTTATGCCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCCAGCCTGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTC[G/A]AAAGTATTTGAGACCAAAAGGAGGT
stSG1345 b	60 G A ---			AACTGACGTATCACAGGGGCAAGTATCTGTCTATAAATTTGAACCTAGTTTGTCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1345 a	54 T G ---			AACTGACGTATCACAGGGGCAAGTATCTGTCTATAAATTTGAACCTAGTTTGTCTTACGGGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1385 b	117 T G ---			TTAATGTCATCCAGGGGGGCCAGGGATGGAGGGGAGGGTTGAGGAGCGAGAGGCAGTTATTTT TGGGTGGGATTCACCACITTTCCCATGAAGAGGGGAGACTTGGTATTTG[T/G]TCAATCATTAAAGAA GACAAAGGGTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCTGTCG
stSG139	69 T C ---			TCGTCTCTTCCAGTGCTTCTGCCAGAAGCATCCCCATGATTTGTGACCCGCACAGCACTTTGTGCT T[C/G]CTTTGAGCACTTGCCACTCTGGCTGGTGTCTGCCACTGATTTGTACTGTCTTGCTGCC
stSG1427	103 T C ---			GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCATCCCT TGCTCTCCACTTCCAGTTTGGCTTCTGCTCTCAIT/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1471	50 A G ---			CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTTAGGTCC[G/G]CTCCCTTGCATGA AATGTGGGAGAGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1483	44 T C ---			CAAAACCAAAATCCTCCACGATATATTACTATTAGTCTAAGT/CJTTTAAATCAAAAGTTGAGA ATGACGAATTCAGAATTTCTTTCATACATAAATTGCTTTCCTTAGTTCTGCAGATGGGTA
stSG1696	67 C G ---			CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGCA [C/G]AATGTGGAGGATGTCTGTTGAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGGAA AATGCCTGA

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGCT TCAAACACAAC TG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCCTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGC TTCAAACACAAC TG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTGACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACT[G/G]GCCACCACCTTCTCTCCGGTCTCCCAAGTACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTTAACATTAAATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAACACAGGCCCTTTGTTGT TGTTATTTTCTCCCTACAATAATTCCTGACTCTGTAGGACAGTGGGCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---	---	AAACGTTGTCCCAAAATGTGTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACACTTAAGAATAATTTTGACATT[C/G]ACATCACAGTGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTCGCGAATTGGCAGCTCCAACCAAAAAATGATTGAGGGGCTCCACAGAGA GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGCGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTCGCGAATTGGCAGCTCCAACCAAAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAAGCAAGCAGCGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTAAACAAATGACTGCGGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACCTGGCATGGCGATGGTCAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATTCTGTGTGCTG
stSG2141 a	113 C T ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTCTATTATTTAAACAAATGACTGCGGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACCTGG[C/T]ATGGCGATGGTCAGGTG GGTGCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAGAAAGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATTCTGTGTGCTG

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s1SG2148	50	A G ---			---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTCTA/GJAAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
s1SG2175	68	C T ---			---	CTCAATGAGGACTCCATCAGCCAAGCGGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGTGCT [C/T]GCCCGGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGAGTGGAAAGGACCA
s1SG2189	41	C T ---			---	CAAGTGGTGAAGCTGGGATTTGAGCCTGATATTCACACTA/C/TCTACATTCCTCCAGTATAATA GGAACTCATCGCTAACCTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTATCTCAATCCTACTC CAGCTTGGCAAC
s1SG2200	49	T C ---			---	TGTTGATGACCATAGAGGATGCAAAAGCTCCGGGTGTTCTGTATGATG/T/C]TTTATATTTATGTAT AATGTCCTTACCTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
s1SG2243	85	G T ---			---	CATTTCTGCTCTGCTTCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAATAAAGTATCAA GATGGTCAGTAGAAAAG/G/TJAGAGCATCTCCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
s1SG2257	65	A C ---			---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAAACTCTGTGAGGCAGGCTATCAGAAGGGCAG/A/ C/TGTGAGGAACCTCGCAAGCACTGGGCTGCTGCTCAGGCAGAAATTTCTTCCT
s1SG2306	67	A G ---			---	GTCATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACGTGTTTCACAG TTCTCCAGAGA
s1SG2334	70	T G ---			---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAAGAAAAAATCCCCGCAAAAAACA AAAAA[T/G]JGCGAGTGAGGGGGCTGTGGAGGGGTGAATG
s1SG2339	63	T C ---			---	AGAGCAGAATGGTGAATCAACAAGACCTCAAAATTTGCTTGACTGCAGAAGTAACGTGTGCAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGTCTATTCIGGCTGTGCTTCCATTATCA
s1SG2465	76	C T ---			---	CAAGACTAAGAAGCCGCAACCGAGTGGTCCCACTCAAAAAGAGATTTCTGATTTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAGTGGGGTATGCA
s1SG2549	140	T C ---			---	TTGCAGGCTTGATTCCACAATAACAAAGTCATGTATAGAGAAATGTGAAATGATACTTGAAACCCAA GATATATAAATATTGAAGTCATTTATGCCCTTTGATGACTGGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACCCACCCCTTTTAACT
s1SG2577	123	T G ---			---	AATTGCCAAATGGAAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTGCAATCCAGTTTGGT CCCAATATAGGCCTCTGCAAGAAGAGATCAATGCCGAACCGAAGTGTGAAAGCA[T/G]GAACAATC CCGGCCAGATTAATTAT

stSG2577	121	C T ---			AATTGCCAAATGGAAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATTCGCCAGTTTGGTCCCAATATAGGCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAG[C/T]ATGAACAATCCGGCCAGATTAAATTAT
stSG2700	58	G A ---			ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAACGTGTCGGGCCCC[G/A]AGTCACTCAGCGTTTCGGGAAATAAACCACCTGGTCCAGAGCAGAGGAAGGCTACTTGAGCCGGACACCA
stSG2724	101	T G ---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTGCTTTTATATTAATATTTGCAATGTCTATAATTTAATACTTATATCCAAATGCTTGCATAATCA[T/G]TTTTTTTAACTCTGGGGTGTGAAAGAAC
stSG2776	65	G A ---			GTGGCCGATCTTTACTTTTCCAGAAAAGGCGGTAAATAAAAACCTGTAGAAAGTCTCGAATATGC[G/A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCCACAAAAATATCCACTAATCCCGAATATAGTAACCCCTGCTTGTCGGAATG
stSG2791	109	G T ---			AAGGAAAGGTGGAGGGAAGAAGGGAAGAAATTACAAATGGTTAGAAAAGAGCAACTAAAGATTATTCATTATACCTCTGAACGGTAACTAGCAATTTTAATAATATTT[G/T]GGGTCCACTTTAAATCTATTAAGCAGAAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791	100	A G ---			AAGGAAAGGTGGAGGGAAGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTCATTATACCTCTGAACGGTAACTAGCAATTTTAATAATATTT[G/T]GGGTCCACTTTAAATCTATTAAGCAGAAAAGTGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85	C T ---			CCGCAATTTTCAACACACATCTATGAAAACTAAGGTGGATCATGTACAAACACAAAAACAAGCTCCCTCCCTCCAAACAA[C/T]GAACAAAAATAAGAAAAGAAACCCATGAATGCCCAGGTTTATATTTTTTCC
stSG2850	88	G A ---			ATGGGTGCATTGTAAAAGGCAATTAATACTTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGATGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCCTCCCAT
stSG3031	71	T C ---			ATACTACGGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCCCTGGCATTTTCTGTGGTGCAGCAA[T/C]GCCCCTTATTTAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A ---			GTCCCAACTCCTCTCCTCTTAGAGAAAAAAGTGTGATTACCTCAACTTGAATATGAAACTGTGATTGAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAAGGCAAACTGGCTGAGGC
stSG3092	94	T G ---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTTGTCACATTTGAAAAACAAGCCAAAGTTCCAAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTCTTATGTTCCAGCCCCCTACTTTAGTT
stSG3230	95	A G ---			AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTGAGATACGAGCACCTGCATCTTTTAGTCAATTGTCAGTGGAGTC[A/G]GTGGGGTGCTAAGTGTCTGAACTGAAGTAG
stSG3245	160	G C ---			ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCCCCAGGTATGTGTAGAGGCCAGTGGGGGTGGCCACTTGGTGTTCACACCCCCCTGCCATCCAGTCTGGCCCCAGTACCTACCTGGGAGGTT[G/C]GTACTTGGCTTAAGTACTTCATGCTTTAT

stSG3265	42 T C ---			AGGTGAATGAGTTACTAAATGTAGCATTTATTATAAGGAA[T/C]GCATTGTGAATAGTTTCTCAG TTTTCAATTATGGAAGATGATGATTTTACGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTTCAGTACAATGGAGGACAGCTTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141 C T ---			TGTACTTACTGTGTCATCCTATCCATTCCCTTCCCTGAGCCTGGACTGCTCTTCCAAAGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]GTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3269 a	24 A G ---			TGTACTTACTGTGTCATCCTATCC[A/G]TCCCTTCCCTGAGCCTGGACTGCTCTTCCAAAGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
stSG3284	130 C T ---			TAACTCAAGAACTTTTCAGTTACAGGAAGATTTATCTAATATTAAAAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATA TTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTAAATGCTGTAAATGGGACATTTGTGTTTGTATCTACCC
stSG3292	99 A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAAATAGCATTTTCTTAACCTCAA
stSG3323	26 C A ---			TAAATGTCATATCTTTAGCTCTCACT[C/A]CCAGTGTATCCATTTTCCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCCTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTTCGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGTTCATTCCTTTTAA
stSG3369	69 C T ---			GATCCCCAGTATTTTCTAAATTGAACCTGTTTGTGGAAATAAAAAATCTGAGGACCACCTCAGAG GG[C/T]ATAAGGGAACCTCTTTGCTTAGTTTCAAGGACTTTTCT
stSG3398	125 G T ---			CAAGACTGTAAGAAACGTAGGCCCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAAGGAATGACATTTCCAAACTGTCAACCTTTGTAGC[G/T]CTGGGT CAAAAGTCTAAAGAGGACAATAAATAGAGACT
stSG3416 a	43 A G ---			TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3424	173 T A ---			GTAAGACAAGGTTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCCTTGGCTTCAAGCGACCGTACCA CCTTGGCCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCGCCGACTTTTAAACTGAAT GTTGAAAATCATCTGCTCTTTGCTGGGTAACTGAT[A/C]AAGTTGCTTAACTTTGTGAAACCCAG TTTCCCTTATCTGTAAACAAAATGGACAAACAGAACTTTTTCCTTTTCTCTC
stSG3436	88 T A ---			GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTGAGGTGATGTGATGGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCC[T/A]GAAATAGCTTACTCTGTTTCTCTATC

stSG3463	103	C T ---	---	GATACAGAAGATAGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTTATTTG AAATAAACAAAAATGCATACACAGCTCAATGGGTAC[C/T]TGGAAACAAACTTGGCTTGAATAATTA CTGA
stSG3491	71	G A ---	---	CAAGATACCTTCATTGCTCTAAGTAGTGCAGTGTGGCAATATTTCTCACGAACAAAGGACGATTTG AAGA[G/A]GTGGAAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTACTGGCACCTGTGGATTCTATTAACTCAITTTACTATTTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33	C T ---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTTTA[C/T]GCATATATGTGTGTACAAACACACACACACC CCTAATTCCTCAAAATGCTCTGGCATAAGTTTTATCTCTACTGGTCTC
stSG3536	213	A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGTACAAAACCCAAATACAGAATGGCTTC TGTGATACTGGCCTTGTGAAACGGCATCTCACTGTCAITCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAG[G/T]CCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
stSG3583	112	G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCCAAAACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586	60	G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTATAAAATTTAAAAATCAGGTGTGGTG[G/C]JACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
stSG3589	101	T C ---	---	ATATAGTCTGTGTAGCAATTATAAATCTCTTTAAAGCAATCTGGCCATATCAAGGCAAAAAAAGT GTATATACCACTTGGCACAAAAACCCCAATGA[T/C]CCTATTTCCAAAGATGTATCCAGATGAAA GTATCCAACAACAAAAAGCTATATACAC
stSG3590	70	A T ---	---	GAGAGATGAGCTATTTATTTCTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTCTAAAAAAA AAA[A/T]TTTCTCTGATGCTCTTGACCCGTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78	A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40	T C ---	---	ACATATGTAACCTGCCATTAGTCCCATATTTAGGATGAGAT[C/G]GGATTGAGAGGCGCATGAACCAAGG ATCGGTAATAATCATTATGAATAATAAGTTATCTGGGAAACGGCCATTTGTCCACATTTACTAA GTGCCTACTA
stSG3646	70	G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATTAACCTTTGATACTTGGTTAAGATGGTGCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATATAACAATA[A/G]TATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCAIT CTTCCTTTTGTGA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCAIT CTTCCTTTTGTGA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCCCTCTGAAAGCCGATGACCATCCAACCCTGGACTCACCT GAAATATCCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCTGGTGTCC[C/C]/TTCTGAAAGCCGATGACCATCCAACCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3698 b	145 G A ---	---	TCCTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCCTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCCAGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTATTGCCAGAGGAGTCCACAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGGCATCCCTGGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACCAGCCAAACAGCAACAGCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAAGAAACACAAATCCACAGGAACAATCTATGTTTCATACCTTTTAGAAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAAGAAATCCACATCATTTGTTGGTAGCAGAGATCTCTTA[T/A]AAAGTTCCCTAAGA CACTGAGGGCATAAAACCAACAAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCTCT
stSG3880 b	115 G C ---	---	GACAAGGGGAAGAGATGCCACAGACACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCCAGGGGC CACCACACGTCTGTGGTCAAGGCCCTCTCTGCGGAGCAGGTTA[G/C]GGCAGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCCCT

stSG3880 a	36 GC ---	---	GACAAGGGAAGAGATGCGCCAGAGACCAGGGCTG/C/GCGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGCCCTCCTCTGGGAGCAGGTCTAGGCACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTTCGCCCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTG/G/GTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAAATTAGTGTATCACCATGGGAACAAGATGCTGATTCTGTCACACTG AAAAAT
stSG3902	104 TC ---	---	TCGTGTGAGACTGGAGAGACCAGGTACCAAGCACCAGCTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTTCTTTCT/C/T/CAGCTCAATAGCTTAACATCTAATTC ATGTTTGCTCCCTTTGCTGGACAAT
stSG3935	50 GA ---	---	GGGTGTCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC/G/A/CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAGTGTCTGA/G/G/AAATATATTTAAGATTTCCCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTTAGAAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCCA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCTC/G/G/TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCACACTGCTTACA
stSG4033	123 TC ---	---	AGAAGCCTTGGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTT/C/T/GTGAAC AGGTGGGCAACAC
stSG4038 a	29 GA ---	---	GCTGAGAGCAGGTGTACAGCCACGCCTGTG/A/JCGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCCCTCAGTCAGGAGGTTCAAGGCTCCCGGAGAGCACTGAGGGTCCACT
stSG406	53 TC ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAAGCTAAACGAACAATA/C/G/GTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAGAGATTATTAACTTTTATCAGGGTGT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 GT ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTGAGATACTATTGTCTGTCTAGATGTATTAG/G/T/ATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATGGCCCTTCATCCTGG
stSG4095 a	27 AC ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTG/C/G/GATACATTTGCTGTCTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATGGCCCTTCATCCTGG
stSG4120	65 GA ---	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC/G/ A/CTTTTCCCCTCAGAGAGGCCCCACAGTTAAACACGTTCCAGCACACCAATTATCCACCGAGCT

stSG4128	54 A G ---	---	CTTGGCAGATAAGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCTT[A/G]TATATTATTT TACTTCTTCTGAAATGCCACATAATTTGCAATAAATGATTCACTCCTTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAAGC AGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACTTGCAGAGGCCGCACTCCCTC[G/A]GC AGGGGACACACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAA[G /A]CAGGCCCGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGACACACGAGGCGACAGGTGCTTTGATGCCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACCAAGAGC[G/A]CCACGGCCGGGACTCCCGGATGGCTGGGGGG GCTATGGCTCTGACAAAGGATGAGCGAGGGCGGGGCTGCCTCCTCCCCCAGGGGCGAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCAT TTAAGCAAAATAAATT/GIAGCTTCTGAGTAGTGTCCAGITTCACCCAAACATTTTG
stSG4331 b	71 T G ---	---	CTCACAAGGCCAACACAGAAAAGATACAAATACATTATCCAGCTAATATTTAGTTTTATGACAC AGAGT[G]TTTTCAAAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAGTTTAAGTTATCACTT GGAGAGCAGATTCTTGGCTCGCCCTTGATTTCTGTTTGAAGGGGTGTGC
stSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TTCCCAACCATTGAGTGACAGAGCTCAGTCAATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGGATAAAGTCACTCTTTTG[C/A]CCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361 a	24 T C ---	---	TTCCCAACCATTGAGTGACAGAGCTT/CJAGTCAATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAAGTCTTGGAATTTCCATAAGGGATAAAGTCACTCTTTTGACCTTCACAACCTAGAAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376	73 A G ---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGCTTCTCCAAGGGGAG AACAG[A/G]CTGGAACTCGGGCTCTGCAGAAGGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTT[C]/CJTCAGTCTTGTAGT ATCCACAGTAGTGATGCTGTGTCATGTACAAAGTGTGTCTGCCAGAACACCCATTAAATTCATGCC
stSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTGCATCCGATATTTTTGCCCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAAACCCGC[A/G]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65	C T ---	---	AGCAGATCAGTCAGCCACCTTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA[C/
stSG4430				T]GTATGCAATGAGAAATAACCAACTGGTAGATGGGGAGGGGAGGCAGGGAATAGGCAC
a	54	A G ---	---	AAATGGAATCTATCTGCTGGCTGTCTCTCTCAGGTC
stSG4448	99	G A ---	---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTTCTATAAGGT[A/G]ATTAAACATA
				GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATGAGGCATCAAGAGGGCCATTTT
				CCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCCTCCCTCCGCCCCCAAAAAA
stSG4449	92	T C ---	---	CGCCTAGCCCTGCCCTCTGGGTCACCTG[G]ATGGGTTAGGCCCTCCCAAAAAA
				ATTAGCCATTTCATCTTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
				TAACTTTGGACAACITAAAACCTA[T/C]TAGTGACATTGCTGTCTAATAATCAATACTTTCATCATA
				GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
stSG4467	42	C A ---	---	CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCCTCA[C/A]AGATGATGTCCATGTTTGTGT
				GAATGAACTCAAACTCTTCAGTTTTTAGAGTCACTTTCTGGTATCGAGCGACACACCGAGGAG
stSG4475	21	A C ---	---	CACACCTGCTCCAAGGCTGCTGCCCTCTGCACACAGT
				ACATGTCACTTCTGACCCAGG[A/C]TATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
stSG4477	32	A G ---	---	TTAAGAGACACAACTGGACITTTTGTCTTTTACTGTAGCACCCAGGTTTCATG
				GTAACATTCTGGGGTGGGGTGAGACAAACA[A/G]ATGAACCAATAATTAATTAACAATTATACATT
				TCAAGGAGACTTTTAACTAGGTTAATGTGAACCGCAGCCATCAATGGTTGTCAGGAAAAAGGGAGA
				TGAAGTCTTGCTCTGGGCAACGTTTGGCCTCAATTGCAGTCAGACTTGGC
stSG4531	79	C T ---	---	TGAACTCAGAGCTGGTGGGAGCTGCAGCGAGGGGAGGCTGGGGCGCAGATGAGCGCGGGGA
stSG4550	86	G A ---	---	CAGCAGGCGTCG[C/T]GCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTGGACTCGATCT
b				GATTCTCATTGACAGGGGAGACGCTGTTGTCATCAA
stSG4550	85	C G ---	---	TGCATTAAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
a				AAAAGAGACAGTGGGCACC[G/A]CAATTGGAGGGGAAGCGGGGCAGGGTTTTAGAGAAC
				TGCATTAAAGGAATGATACGGCATAATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
stSG4590	47	A G ---	---	AAAAGAGACAGTGGGCAC[C/G]GCAATTGGAGGGGAAGCGGGGCAGGGTTTTAGAGAAC
				AATCAGGCACAAGCTCGGGAGAGAAGCCAAACAAAGCTCTTCTGCAC[A/G]ATGGGAGGGAGACAC
				CATTGAAAAGGCATCGTTCCTTCTTCATGCAAGCGAGGCGCTGGCTCCACAGGCATGGTCTCCTTG
stSG4623	22	T C ---	---	AATCTGTATCACCCAGCGCTGG[T/C]CAATGTACTAGTAGCTTCCACAGGGATTTTTTATACTATTC
				CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTCACATTTATCT
				TAAATTCCTGTCAAGATGCTCTGGAG
				TAAAAAAAACAACCCCCCAAAAAACACCCAGAAGTTTTTGAAGTTTTATGTTTTTTCAGATTTAAAG
stSG4843	102	A C ---	---	GTATTTCTTTCTAGCTTCTAAATTTTGAGTCA[T/C]ATCAGAAAGTCTTCCCTACTCTCAAGGIGA
				GAAAGGA

stSG4850 a	38	C T ---			GGAACTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC/TGTGCACTTGCAGGCCACGTCAAGGAG AGCCAGCGGTCCCTGTGGGGAGGTTTCCAAGGTCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCC
stSG4879	86	A G ---			AACTCTGAAGGGGGTGAACCTCAACCCAGCCCTTGTTCTGTGAGGTCCTGCTTTTGCAGAAATGGCCTG CCCCTGGGACTGGAGCAG/GCTTGGTGAGCTCTAGGTGGAGGGTGGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104	G A ---			ACTGGACTGGCTGGCTTGTGAGCCGGCTGAGCGGCGTGGGACTGCGGCTGACCACCTCGCTCTTCAG AGACTCGCCCGCCGGTGACCAAGACTAGCTCTGCC/GA/GTGGGAAAGCAGAGCAGGACC
stSG4896	112	C T ---			AAACAAATCAACCCCAATCCCAGAGTCTATGTACAGGGCCACTCCCTGCCCTCTCTGCCATAGAGA GGTTGGGGGCAGCTGAGGAGTGGTGGGGCTGGGCACCTTTTCTT/CAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22	G A ---			ACAGTGCCGATGGTTACACAA/TG/AJTGTAAATGTATTTAATCCCACCTTACGAATGATTAAATGA TAAATCTTATGTTTATTCATCACTACCAAAAGGCTGTGGTGACGGGTGCTGGTTCTGTGCTCT
stSG4950	24	A G ---			TCATGACTCCAGGAAAAGGTCTT/GTCTTAGCTTCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136	G A ---			AGATACGGGCAAAACACTGGGATGGCTTCTTGACAACTTAAGAGGTCTCGAGTTATATTCTGGTT GGGAAACACTGACCCAGCCCTTATTCCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTTCATGAGCC CC/GA/GTGACACAGATGGGGCCCTGCTCTATATCAAC
stSG4961	91	C T ---			GAAGTGCTCTGAGGAGGTGACTCTCCCTGGCTGACAGGGGAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72	A G ---			ACTGGTGCCTCTCAGCAGATTCAGGGGTCTGTCAGGGCTGGTTACCAAACTCAGTAGGAGTGCAA GGGCT/GJTACCCCGGAGCTAGACAGCCTGGGTTGAATCTCAACTTCTCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22	T C ---			CAAAGGAGAGTAGGAGCCCCAA/T/CJTJTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAT
stSG6312	37	C T ---			ACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/C/TJATGCCATGCGGGAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107	G A ---			GCTCTGGTCAAGCAATTTCTCCAGGACAGAAGCAACAAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTTGTCCAC/G/ATAGTTCAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAAACATTTGCTCTTTGGCCTGGTGTGACAGAAAGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG

stSG6362	88 G C ---	---	TGTGAAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAAGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAGGAAGGAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62 G T ---	---	CACATCTGTGTTTCTGGAGCAAAGGAAACCACAGAAAGGCCAGGAGTTTGGGTGTGCACCTGG[G/T]T GTCTTTCAACTGGGTGGAACCAACTGAGTCCTTGAAGTCTCGCTCCTGAGGCTGCAGAAAGAATAGA TGGCTT
stSG8022	53 G A ---	---	AGTCCTGACTCCCTGTTCAGTGACGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAAACTGGAAACTCTACAAATCAATGCGTTTATTTCTTTATTTTCAGAGGCGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67 G C ---	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTTACTTCCAAAGAAATTCAGAAAAATTTGTGTGTT G/CITGGGAGGCAGGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGTTGGTAAAA
stSG8064 b	46 C A ---	---	AGCTGGCTCTTCTTCTGTGCGTGTTCGGGAGGCTTCACGTCCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8064 a	23 G C ---	---	AGCTGGCTCTTCTTCTGTGCGTGTTCGGGAGGCTTCACGTCCTCGCCGCTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8072	59 A G ---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGTCTTGTGTCTTAGGG[A/G]TGGC AGAGGCAGAAGGAAGTCCGAGTATTAGTGGCCGCAATGCAGTTCAAGCCTGTGTCTTCAAAA
stSG8100	40 A G ---	---	ATACACCCACACACCCCACTCAACCTTGTATCAAAATTC[A/G]AAGTGTAACTAAAGTATAAGAAT ATCATGACTAGTTAAAGATAGCAATACCATAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCCTTGGAAATGGG
stSG8102	138 T C ---	---	AAGGCTCCTTTGAAAGCATGGTTTATTGTTCATTAACTTGTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGACATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAAATGTGAAA TGA[T/C]TGTATAATCAATAATCAATAATTGGTATTGGTTTAGGAAATGTGATGGT
stSG8105	110 A G ---	---	CAGTGGTCTCAAACTCCAGCGTACACGAGGATGGTCTTGTGCTTGTAAATACACAGATGACTAGGCC CACCTGCGGAGTTCCTGTTGGAGTCTAGGCCTGAGAAATTC[A/G]TTTCTAACAAAGTCCCAGGTGA CCCTGAGGCTCTTGGACTGGGAACATGCTTTGAG
stSG8130 b	96 T C ---	---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGACTGGATGGTGGCTGCTTTTAAAGTTCAAATT GACATTCAGACAAGCGGTGCGCTGAGCCTT[C/G]TGCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36 C G ---	---	GTGTGTACATCATTTGGGAATGGAGGAAATAAATGA[C/G]TGGATGGTGGCTGCTTTTAAAGTTCA AATTGACATTCAGACAAGCGGTGCGCTGAGCCTGTGCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124 T A ---	---	TTGTGGACTTCAAAATCTTCTTCAGATTTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAAATTTGTGAACACAAATCTAAGAAATGAATGAGATGT[T/A]CTGAAA TCTGATTCAACACCTTATCTTAACTGACTTCTGTCAATCCTCTGTCTGTGAAGG

[illegible]

ESTD-AT3a	--	--	--	---	---	AGACCTCAGTTTCCTTCTGTATAAAGGGGAAGTTTGTTCTTGGATCTCCATGGGCCACAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGAGGAATTTGAAAGGGCATTTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAAATGTGG
ESTD-B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGGAGCGGCCCTAGCCGGGGCCCTCTCTGGGCTGGGGTGTCTGGCCACC GTGGAGGCAACCTGCTGGTCACTGTGGCCATCGCCCGGACTCCGAGACTCCAGAGACCATGACCAACGTT GTTCTGACTTCGCTGGCCGACGCGACCTGGTGATGGGACTCTCTGGTGGTCCGCGCGGGCCACCTTT GGGGC
ESTD-BA511	--	--	--	---	---	GGGCAACATAGTGAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAAGATGGTGCCACTGCA
ESTD-BCL2	--	--	--	---	---	AGCTGGATTATAACTCTCTTCTTCTCTGGGGCCGTGGGGTGGGAGCTGGGGGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAACAGGGTACGACAAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATCGGGGAGATGTGG GGCGCGCCCCGGGGGGCCCCCGCACCGGGCATCTTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA GACCAAAGAGGTCACTTCTGTGTTCCCGGAAGGGAGGCGAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTCTGGCACA
ESTD-BRCA1a	--	--	--	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCCAAAGATCTCATGTTAA GTGGAGAAAGGGTTTTCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCCAAAAACAGAA CCAAATAAAAT
ESTD-BRCA1b	--	--	--	---	---	ACTAAATGTAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAAGAGAA ATGGGAAATGAGAACATTCCAAAGTACAGTGAGCAGCAAAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTGCTGAAAAATGACATTAAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGGCCAAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTAAATTTGCTCCGGGAAGCACATTTCATCAA CCCAGTCAGTTTGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCTTTCAACCATGCATTCATCTCAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	

ESTD-D7S399	--	--	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTTACAAAACATTTTCATCCATGGACTCCATACTAG AATAATTTGAAGAAACAACATGACAAAACATTTTC
ESTD-DM	--	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGTGTGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGAGCTGCTTCCAAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD1	--	--	--	---	---	---	TCCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTCGAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAAACTAAGGTAC
ESTD-DRD2	--	--	--	---	---	---	TCTGCCTTTGGTGAGGAGGCTGCCCGGGAGCCCCAGGAGCTGGAGATGGAGATGCTCTCCAGCAACA GCCACCCGAGAGGACCCGGTACAGCCCCATCCACCCAGCCACCAAGCTGACTCTCCCCGACCCCG TCCACCAAGGCTCTCCACAGCACTCCGACAGCCCCCGCAACACAGAGAAGATGGGCATGCCAAAG ACCAACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	--	--	--	---	---	---	AAGACGATGGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGCTGGCTGG CACCTGTGGAGTTCTGTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD-ERB2	--	--	--	---	---	---	TCTTCAGGATCCGCATCTGCGCCTGGTGGGCATCGCTCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCAGTGCCGGGGGGCGGTGCAGACCCACGCGGCTGGGAGGACTTCACCC CGCCTCACCTCCGTTTCTGCAGCAGTCTCCGCATCGTGTACT
ESTD-ETS2	--	--	--	---	---	---	ACTCACAGTGTCTTTAAGTGAAAATGGTCGAGAAAGAGGCCACCAGGAAGCCGTCCTGGCGCTGGCA GTCCGTGGGACGGGATGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGGACACACAC AGACTATTTTAGATTTCTTTTGGCTTTTGCAACCAAGAACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTCTTTCAGAAAGTTAGTTTG
ESTD-F2	--	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTTACAGTTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTGTGTAAAGTATGATGTTTAAGTCAAACTTCATTTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC

ESTD- GDH	--	--	--	---	---	CGCAGACCGGTACGTGTGGGGTCGGGAGTGTGGAGGGAAGGAGGGAAGTGGGGTTAGGGACT TTCCGGGTGACTTTCCCGTTCTGTCTTCAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTCGACCGTGTCTGTGTCGCCCTGTTACAGTGTCTGTCTGCGGACGTCGA CTGTGTCGCCGGAATTCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTATGATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTTGGTCACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCOCACCCACACCTGGCTGG AGCAGGAATGCCAGGCGCGCTGAGCCCGAGGAGCAGGCTAGGATGTGAGAGACACAGTCACCC TGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	GACCCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACAGGCATCATTG AAACCAAGTTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTTCATCTCGGGTCTCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HFRAS	--	--	--	---	---	CTGGGCTGCCCCGAGAGCTGTGGCACTGTGACGGCGCGCCAGGCTCAOCTCTATAGTGGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGAAAGTTCTCCACTGTTAACCAGTCTATGTTGGCAATGTGGCTGGGCCACATCTGCGCCTTG AGGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTACCAAAAGCTATGATAACCTTAATACACCTGAGCAAGAGTTCGGCCCTCCGGCTTGATTCC AGATGGAGCTTCTCTTATCCCTGATGATGATTGGCTTCCTGCTG
ESTD-HT2	--	--	--	---	---	GGGTAAATTTCCGAGCACTTTGCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTGTGACAGAGATAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTGTGAAGTTTCAAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAACGAGCCGGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGGTGCTTCTATCGCAAGAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACAGCCCCCAAGAGTCACTGAGACTGGCAGCTTCTGACGAGCGGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGGCGCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACACAAGCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGTGTGTTTCTTCCCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGATGTTAGCTTGAGTAAATTCAGGATATCTCTCTACAAAATGAAA ACATTTCTGTGCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAATGTTT CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	---	---	---	---	TTTACTATTTCATGGATACAGAAATTGTGGGAGTCACTATATTCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACCTGAAAGT ATGTAATACTTCACAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	---	---	---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTTATTTTATTTTG AGATGGAGTCTGGCTCTGTACCCAGGCTGGAGTGAGTGCGACAACTCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCTCTGCTGCTCAGCCTCCGAGTAGCTGGGAATACAGGCCACCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCACCGT
ESTD-IL1B	--	---	---	---	---	CCACTTACAGATGGATAAATGGGTACAAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATGAGGGTGT GGGTCTCTACCTGGGTGCTGTCTCTGCTCAGGAGCTCTCTGCAATTGCAGG
ESTD- KRT10	--	---	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCATTTTAAAGTAAGTAACTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	---	---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAATCTCTCCAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGCCAGATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCATCTCTCCGCTCAGGTTTACCAGCTCAACATTGACACA
ESTD- LF79	--	---	---	---	---	GGGTGATTTTGAGGCTCAGTTAATATTTCAAAATTTGAACCGTAGCAAAACTGCATTGGTATTAGA AAAAATAAAATTTCCAATATGTAGTGTGTGTATACCTGCTGCCATGCAGCATCATAGCCTGT GGAAACCAGGAGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	---	---	---	---	TACACACTTTCCTTACCCTTCACTGAAAACGACTCGCAAACTGGAGCCTGTAGGAATGGAGTTGA CCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	---	---	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGTTTGTCTTAATCTCAATCAATGTCTCTCACTTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACAACAATTTATAAAATTTTTCACCTG
ESTD-MCC	--	---	---	---	---	TTGTCAGGAGTGTGTGATGCTGCTGCCAGCTGTCTGCCAGTCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTGTCTTTCCAAAGGTTTGGTCTAAGTGTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATG
ESTD- METH	--	---	---	---	---	ATTATCCAGATGAATTTACAAAATATACCAGATCCACAGACTGATATGGCTGGT
ESTD-NF1	--	---	---	---	---	

ESTD- NFKB1	--	--	---	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTTCTAAAAAAGAAAAAGAAAA AAATTTAAAGGGTGACTATATCCACACTGCACACTGCCTAGCCCAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATTTCTGAG AAACTTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAGGTTATCA TGTCCTTAGGCCAGCCCTGCTTGCTCCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NPPA	--	--	---	---	---	GGAGGAGGAGGTGGGAGGGGCTGTCTGCTCCAGGTCCACAGACCAGAGAAGCGGCTCAGTG TATCCCAACCCCAATGTGGGCTGGGAGATGAAGAGGAGTTGATGCAGGT GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTCAGGCATATAGAATTTGGT GGGTTTTCTTTATGTAGGGTGATTTGGATCTTTTGTGTTGATTATATAGCAATTTGAGGG ACAAACCATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTTGC ATTCCCTGTGGTTTTTAATAAAAT
ESTD- OTC	--	--	---	---	---	GTGACCTTCTCATTAAAAAATTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGTATGTAACA GCCACCACCCACCCAGCACACCTCCACCTCAGCCAGCAAGTTGTTGACACAAGAGAGCCCC TCAGGGCACAGAGAGTCTGGACACGTGGGAGTCAGCCGTGATCATCGAGGCGCGCGGCAC ATGGCAGGATGAGGAAAGACCAAGAGTCTCTGTTGGGCCAAGTCTTAGACAGACAAAACCTAG ACAATCACGTGGCTGGCT
ESTD- PA11	--	--	---	---	---	CTCTCAGGAACCCAGTCTTCTTACCAACACGACTTATGCTGCCGAGAGGTACAACCCGTAGA ACTTCTTCTTAAGTAAATTTAGTTAAAGGAATCGAACTGGCTCTGAAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTTCACCTTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCCC CCTTCTCATGCCAGATGGAATCCAGTCCCTCAGGATCTGCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAGGGCAGGACTAATCCAAATCTTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGGTGGCAACATTGAAAGCCTCGTACC GGGAGTAAACCTGGATTGGGAGATTTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAATAGCCTATTTCTGAGCCATATTAATTTGTTGTGCCCTTACATT ATTACTCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAAATCTCCATCACCTTTGGGCTTGT CTACTTTGCCACAGATTATCTTGTA
ESTD- PS-1	--	--	---	---	---	ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAGAGCGAGCTGTGGTGACAAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGTGCCCTAGAACATTTGTAAAGAGGTAAAGTCTTATGAAATTTATAATCTT ACCTACAGACGCTGCTGGATGGTGTGTCACACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG CTGGAGAGAGCGTGGCGGAGACCTGGAAGGCT
ESTD- PMP1	--	--	---	---	---	
ESTD- PerrDS	--	--	---	---	---	

ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGGCTGGCTGCTGGAGAAAGAGCGTGCCGGAGACCTTGAAGG CCCTTCTGGAGAGTGTGAAGAGCTGGGCAAGGCAACAGGTGGAAGCCGAGGGCGCAGACGCAGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGCCCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCAACTCCGAAAGTCTGAA
ESTD- RVR1	--	--	--	---	---	CTTCGTGACGGGAGGTACGTCCTCCGCCCTCTTCATGGACATATGGATGAGTGTGACCAATTTCCC CTGCTGACAGTGTATACACAGCGCAGACTTGCTACTATGAGAGGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAATCAGCTGGAGTGGGAGCCACCTGCGCTGGGCCAGGCCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	TGAACACCCCTGTGTCCGGAGCCAGGTGTGTTTCTCCTGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGGCCACCTGCTGTTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCCAAGCCAGTTTCTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	TTCACTTTGTGGATTGTTTCTTTTGTGTGTCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAAG TTTGCTTTGGCTGCCCTGTGCTGTGGGATATTGAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTTCCCAATGTTTCTGTATAATAGTTTCAATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCAATTTATCAGGGCCCATCAGTTCAATCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACTAGAACGTTTGTTTACAACCTTTCTCCAGTATGGATGGGATATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACATCA
ESTD- THPB	--	--	--	---	---	TGCGGCCCTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGAAACAGACCACAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTTGAGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAAGT GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTGTATGCTT GTGTGTCCTCAACTTCCAAATCCCGCCCCCGGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCTCTGTCAGCTTCTGGATTTCTGTTCCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAAGCTGGTGTCTCATGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGTCATCCAGACAAAGAGGTCAATAATATTGATGTCGTTAAACAT GGGTGTTGATCCATTTTCAATTTGGCCATAGGTCCCTATGGGGATGACA

EST11458 6	--	--	--	---	---	CCACITTTGGTAGTCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTTGTCTCGAGITTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCAAAGCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAAACATTCTATGAGCCAGGAGAGAGATTACGTATCTCTGAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGTCTTCCCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	AOCTGGTGTGCTGGTGTGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTOCTGGGGCCCGTGG TCCTCCTGGTGTGGTAGTCTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGGTCCCCAGGTGCGGATGGTCAACCCGACACAAAGGAGAGCGCGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAATATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTGCATACATGATGAGGAGACTGGAACCTGAAAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGCAACAGCAGGTTCACTTACACT GTTCTTAGATGGTGTCTTAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAATGACCGATGGGTGAGAACTGTCTCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAGCCACAGAGCTTGCCAGATC
EST76807 7	--	--	--	---	---	ATGTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGCTCTATCTCCAGCGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG
EST44438 7	--	--	--	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGAACCTCAAGCTCGACTTCAAGGACGTCT GCTCCGAACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAATGATGAGTAAGGGAACCTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACCTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGTCTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	---	---	---	TGCCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTTATCTACTTATGATGATGTTACATTTGGGCTTGACTTCCAAACACGGAGAAG CATTGTTTCTTCGGGCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
EST36751 7	--	--	---	---	---	CCAAAGTCGTTCAATTTAGCTTTGCAAGGTTTTAACTCGATTACTTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTTCTGATCTATGGTTCAAGTTAAACAG
EST40582 --	--	--	---	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAATATTTACCTTTTGAAAAAATAAATG AAGGATTTGACCTGCTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTTGAAACAATACAGAT GCCTTCCCTGTAGCAGTTTTTCAGCCTCCTCTACCCCTA
EST18288 3	--	--	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGACCCCTGGCTTTCAACACCTAGTCCACTTCCAAAGGTAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	---	---	---	TTCCGCCAGCCCCCATCTTGGCACCCCTGGTCCCTCAGGGCCACCCCGGCGCACTCAACCGCTCT CGCTCTCGGTAACATCCGGCCGGCGCGCTCTTGAGCACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCCCGGGCTTGCCAGGGCCAGCCCTGCAGAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	--	--	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAGCCCTAGAAGATACACGAGACCGA ATGTATCAAATGGACATTCAGCAGGAACCTCAACGATACCTGCTCTGTGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	--	--	---	---	---	AGACCATGAAGGAGTTGAAGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCAAGGAGCTGCAGCGCGGCGAGGCCCGGCTGGCGCGACATGGAGGA CGTGGCGGGCGGCTGTGTGAGTACCGCGGCGAGGTGCAGGCCATGCTGGCCAGACACCGAGGAGC TGCGGGTGCGCTCGCTCCACCTGGCGCAAGCTGGTAAAGCGGCTCCTC
EST43211 8	--	--	---	---	---	CGCCTGGTGGAGTACCGGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGCTGCGGGTGCG CCTCGOCTCCACCTGCGCAAGCTGCGTAAGGGGCTCCTCCGCGATGCCGATGACCTGCAGAAAGCGCC TGGCAGTGTACAGCGCGGGCGCGAGGGCGCGAGCGGCTCAGCGGCATCCGCGAGCGGCTG GGGCGCTGGTGAACAGGGCGGCTGGCGGCGCGCCTACTGTGGGCTC
EST36770 1	--	--	---	---	---	TGTAGCCAAAGTCACCTGCATCATTTTGGCTGTGGCAGGCTTGGCCAGTTTGCCAGCTATAATCC ATCGAAATGTATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCGATAGGCTGGGCTGACCAAAATATACTGGGTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATCTCTATTGTGAAGGCCCTAAAGAGGCTTATG

EST65258 8	---	---	---	---	---	TGCCCCATCAGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTACCAATTAACAGAAAT CCAGTTATTTTCCACCCCTCAAATGACAGCCATGGCGCGGTCTTCTGGGGCTCGTCGGGGG ACAGCTCCACTCTGACTGGCACAGCTTTTGACATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG GTTAGGTGGTGTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA ATGCAGGATGAAGGTGGACAGGAGGAGAGGGGCAACCTGTATCCAGGGCTGCAGATGTCGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCATTTGTTTAGCATTACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCCTAAATGCTTATTTAAATGACAGTGGAAG TTTTTTTCCCTCGAAGTGCCAGTATCCAGAGTTTGGTTTTTGAACCTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTTCGICCTGGGGTTTTTGGTGCATGCA GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATCTCCCAATCTGTGCGTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGAA GGAAGAGATTTAAGAAGCTTGATTGGACAATCTGCTTGTGAGTGTGAAGAGTTTCATGTCTCT GCCTGAGTTACAACAGAAATCCTTTAGTACAGCAGGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGTAAGAAAGTAGTTATTTTTTA GGAATATTAATAATATTTAAATACCTCCATTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT ATCACAGGTCTGTGCTGTGGCCATCATTTCTGGGAGAGATGGTGTCTGCAAGCCCTTTGG CAATGTGAGATTGATG AGGAGAAGCTGAGGAGGGGAGAGAGACAAGATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAAATGAC TGAAGCTTCTGCCAGCTTGCTTCTAGGAGAACCCGGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCACATGGCGGGGATGGCGGGAGTTCTGGTCC TGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGCGGTTGCGATGCTAAACCTTTGTTCT TGGCAAGGAGGGGGGTGCCATGCCTGAGATGATAGTGGCGCC Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence
EST38216 3	---	---	---	---	---	
EST62782	---	---	---	---	---	
EST35879 9	---	---	---	---	---	
EST68308 5	---	---	---	---	---	
EST54045 6	---	---	---	---	---	
EST52908 0	---	---	---	---	---	
EST19590	---	---	---	---	---	
EST76136	---	---	---	---	---	
EST58607	---	---	---	---	---	

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.